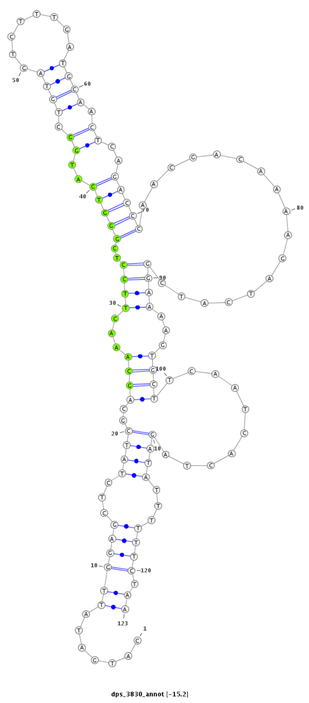
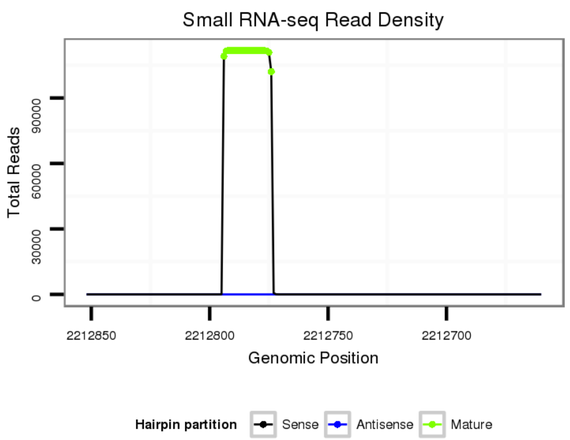
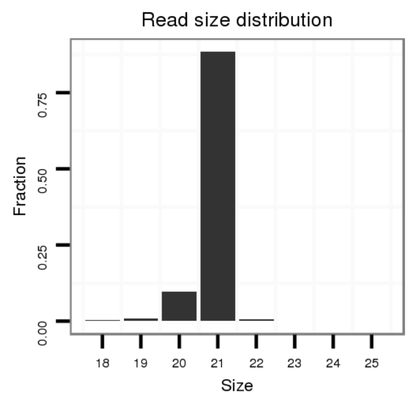
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3830	**4_group5:2212710-2212802 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

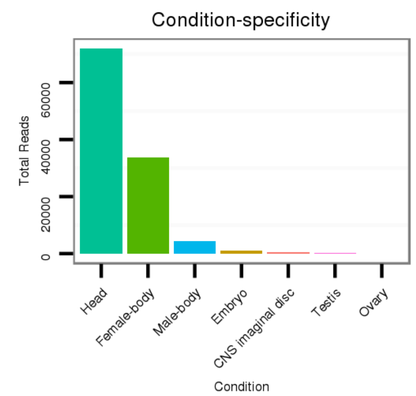
Legend: mature star mismatch in alignment mismatch in read

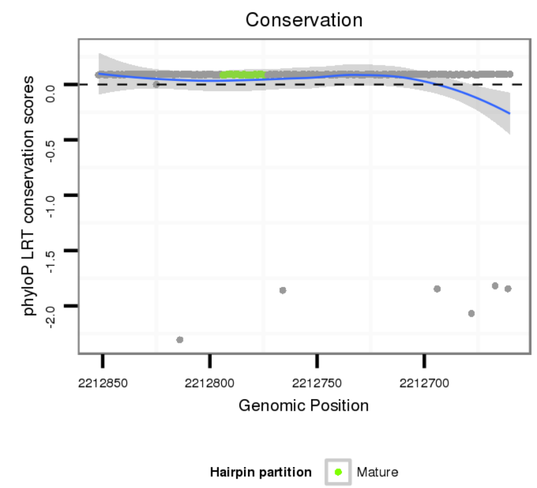
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA28018-in]

No Repeatable elements found

mature	star
1. dps_3830 4_group5:2212774-2212794 - 2. dps-mir-2568b 4_group5:2251160-2251180 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTTCCTTCGTGTCTAATAATTTTTATAAAAAATATTCATGATATTGGAGCTCTATCGCAGCAAACTTCCTCGGGTCATGGCTGTAGTCTTTGATGCAACTCAGACCCAACGACAAAAGATCATCGGAAAAGTGCTTCAATCACTAGATATTTTTTCTAATTTTTCACGTGATCGAGAGCAAAATTTAATTTTTA ********** (structure)	Read size	# Mismatch	Hit Count	Total Norm	Total	M062 head	M040 female body	GSM444067 head	V112 male body	M059 embryo	SRR902012 CNS imaginal disc	GSM343916 embryo	SRR902011 testis	SRR902010 ovaries	M022 male body
.....GCAAACTTCCTCGGGTCATGG.....	21	0	2	98852.50	197705	76881	57773	52047	7769	1117	1084	804	198	27	5
.....GCAAACTTCCTCGGGTCATG.....	20	0	2	8660.00	17320	7966	4696	3782	754	47	29	30	16	0	0
.....CAAACTTCCTCGGGTCATGG.....	20	0	2	2233.50	4467	249	4055	127	29	3	2	1	1	0	0
.....GCAAACTTCCTCGGGTCATGT.....	21	1	2	851.50	1703	999	226	396	67	5	4	0	6	0	0
.....GCAAACTTCCTCGGGTCAT.....	19	0	3	599.67	1799	985	338	456	14	3	1	2	0	0	0
.....GCAAACTTCCTCGGGTCATGGC.....	22	0	2	558.50	1117	586	150	353	10	9	3	6	0	0	0
.....GCAAACTTCCTCGGGTCATGGT.....	22	1	3	382.00	1146	598	108	380	56	3	0	1	0	0	0
.....GCAAACTTCCTCGGGTCATGC.....	21	1	2	355.00	710	587	6	88	4	23	0	2	0	0	0
.....GCAAACTTCCTCGGGTCA.....	18	0	3	270.33	811	581	88	118	0	18	0	4	0	0	2
.....AAACTTCCTCGGGTCATGG.....	19	0	2	222.50	445	142	203	82	15	3	0	0	0	0	0
.....CAAACTTCCTCGGGTCATG.....	19	0	2	161.00	322	10	308	4	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGA.....	21	1	2	130.00	260	146	31	71	7	4	0	1	0	0	0
.....GCAAACTTCCTCGGGTCATGGA.....	22	1	2	119.50	239	113	56	57	4	0	3	0	6	0	0
.....AGCAAACTTCCTCGGGTCATGG.....	22	0	1	85.00	85	23	50	9	2	0	0	1	0	0	0
.....GCAAACTTCCTCGGGTCATGGCTG.....	24	0	2	34.50	69	0	0	69	0	0	0	0	0	0	0
.....CAAACTTCCTCGGGTCATGGC.....	21	0	2	33.50	67	36	20	5	2	1	3	0	0	0	0
.....GCAAACTTCCTCGGGTCATT.....	20	1	4	33.50	134	91	13	28	1	0	1	0	0	0	0
.....GCAAACTTCCTCGGGTCATA.....	20	1	3	29.67	89	73	6	7	2	0	0	1	0	0	0
.....GCAAACTTCCTCGGGTCATGGCT.....	23	0	2	29.50	59	2	0	56	0	0	0	1	0	0	0
.....AACTTCCTCGGGTCATGG.....	18	0	2	20.00	40	6	31	2	1	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCAC.....	19	1	3	18.00	54	53	0	1	0	0	0	0	0	0	0
.....AAACTTCCTCGGGTCATG.....	18	0	2	14.00	28	9	15	4	0	0	0	0	0	0	0
.....CAAACTTCCTCGGGTCATGT.....	20	1	2	10.00	20	0	19	1	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGGG.....	22	1	2	9.00	18	10	6	2	0	0	0	0	0	0	0
.....CAAACTTCCTCGGGTCAT.....	18	0	3	7.67	23	2	21	0	0	0	0	0	0	0	0
.....AGCAAACTTCCTCGGGTCAT.....	20	0	1	6.00	6	1	4	1	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATAA.....	21	2	3	6.00	18	1	0	17	0	0	0	0	0	0	0
.....CAAACTTCCTCGGGTCATGGT.....	21	1	3	5.67	17	4	12	1	0	0	0	0	0	0	0
.....AGCAAACTTCCTCGGGTCATG.....	21	0	1	5.00	5	1	4	0	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGTT.....	22	2	3	4.67	14	8	2	3	0	0	0	0	1	0	0
.....GCAAACTTCCTCGGGTCATGGAA.....	23	2	2	4.50	9	2	5	2	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATTT.....	21	2	4	4.50	18	8	4	6	0	0	0	0	0	0	0
.....ATATTGGAGCTCTATCGCA.....	19	0	1	4.00	4	0	2	1	0	0	0	0	0	0	1
.....GCAAACTTCCTCGGGTCAA.....	19	1	3	4.00	12	4	5	3	0	0	0	0	0	0	0
.....CAAACTTCCTCGGGTCATGGA.....	21	1	2	3.50	7	0	6	1	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGGCTGT.....	25	0	2	3.00	6	0	0	6	0	0	0	0	0	0	0
.....AAACTTCCTCGGGTCATGGC.....	20	0	2	3.00	6	2	1	3	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGAA.....	22	2	2	2.50	5	0	2	3	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCATGGCTGG.....	25	1	2	2.50	5	0	0	5	0	0	0	0	0	0	0
.....GCAAACTTCCTCGGGTCT.....	18	1	4	2.25	9	2	3	4	0	0	0	0	0	0	0
.....AGCAAACTTCCTCGGGTCATGGA.....	23	1	1	2.00	2	0	0	0	0	0	0	0	2	0	0
.....CAAACTTCCTCGGGTCATGGCT.....	22	0	2	2.00	4	0	1	2	1	0	0	0	0	0	0

Anti-sense strand reads

CAAGGAAGCACAGATTATTAAAATATTTTTTATAAGTACTATAACCTCGAGATAGCGTCGTTTGAAGGAGCCCAGTACCGACATCAGAAACTACGTTGAGTCTGGGTTGCTGTTTTCTAGTAGCCTTTTCACGAAGTTAGTGATCTATAAAAAAGATTAAAAAGTGCACTAGCTCTCGTTTTAAATTAAAAAT ********** (structure)	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	V112 male body	SRR902010 ovaries	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group5:2212660-2212852 -	dps_3830	GTTCCTTCGTGTCTAATAATTTTTATAAAAAATATTCATGATATTGGAGCTCTATCGCAGCAAACTTCCTCGGGTCATGGCTGTAGTCTTT----------GATGCAACTCAGACCCAACGACAAAAGATCATCGGAAAAGTGCTTCAATCACTAGATATTTTTTCTAATTTTTCACGTGATCGAGAGCAAAATTTAATTTTTA
droPer2	scaffold_5:6591006-6591227 -	dpe_3	GTTCCTTCGTGTCTAATAATTTTATAA-AAATATTCATCATATTGGAGCTCTATCGCAGCAAACTTCCTCGGGTCATGGCTGTAGTTTTTGAAAGCCCATGGCTCGAGGATGTTGCCTGTGATGCAACTCAGACCCAACGACAAAAGATCATCGGAAAAGTGCTTCAATCACTAGATATTTTTTCTAACCTTTCACGTGATCGATAGCAAAATTTTATTTTAA

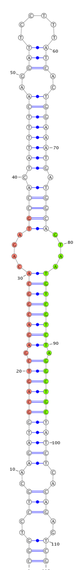
Generated: 09/08/2015 at 08:21 PM

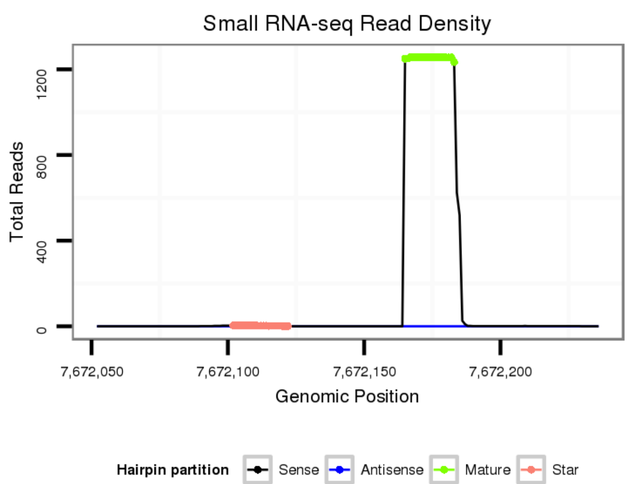
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

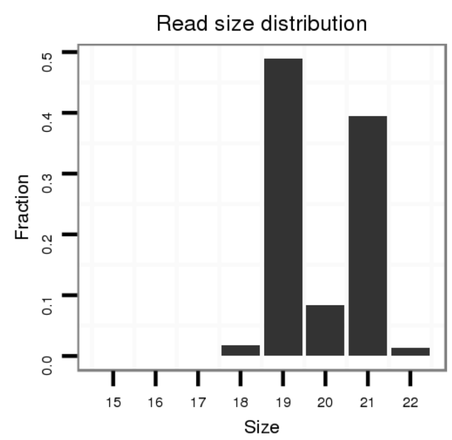
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_27	**4_group3:7672102-7672186 +**	**confident-exception**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

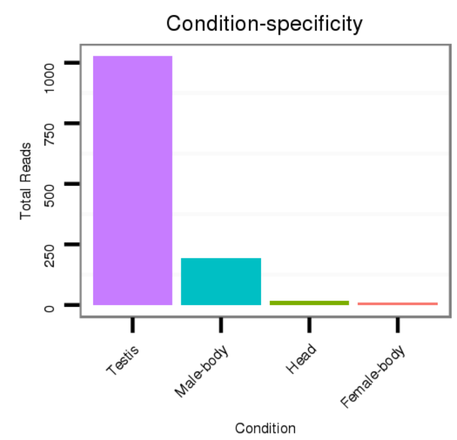
Legend: mature star mismatch in alignment mismatch in read

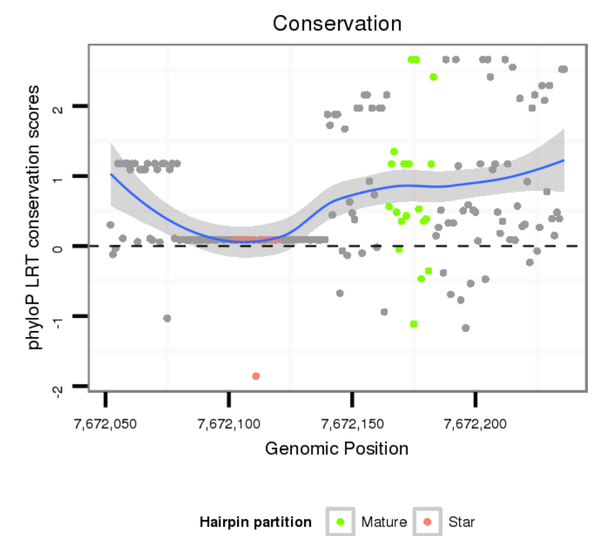
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dpse\GA25667-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATTTTAAAGTTTGCCAGATCCTTTGATACATCCTCCGGTCCTGCAAGATGGCAGTCGAGACGGCACAGATGCCACTATTTTCAAGGATTCCTTTATCACTGGAAATGATGGCAGTAATGTCGTCTAGGCTGCTATCTCACAGAGTCGAAGGACACGAAGGAGTTGTCCGAGGACCTGGCCAACTT **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body	GSM444067 head	M022 male body	M040 female body	M062 head
..GTAATGTCGTCTAGGCTGC	19	0	1	610.00	610	526	63	10	6	5	0
..GTAATGTCGTCTAGGCTGCTA	21	0	1	492.00	492	376	105	4	2	5	0
..GTAATGTCGTCTAGGCTGCT	20	0	1	105.00	105	87	13	0	4	0	1
..GTAATGTCGTCTAGGCTGCTAA	22	1	1	33.00	33	32	1	0	0	0	0
..GTAATGTCGTCTAGGCTGCTT	21	1	1	28.00	28	24	0	0	3	1	0
..GTAATGTCGTCTAGGCTG	18	0	1	22.00	22	21	0	1	0	0	0
..GTAATGTCGTCTAGGCTGCTAT	22	0	1	17.00	17	16	1	0	0	0	0
..GTAATGTCGTCTAGGCTGT	19	1	2	13.00	26	25	1	0	0	0	0
..GTAATGTCGTCTAGGCTGCTATT	23	1	1	7.00	7	7	0	0	0	0	0
..GTAATGTCGTCTAGGCTGCTAAA	23	2	1	7.00	7	7	0	0	0	0	0
..AATGTCGTCTAGGCTGCTATC	21	0	1	4.00	4	4	0	0	0	0	0
..GTAATGTCGTCTAGGCTGCTATC	23	0	1	3.00	3	3	0	0	0	0	0
..GTAATGTCGTCTAGGCTGCA	20	1	1	3.00	3	1	2	0	0	0	0
..GTAATGTCGTCTAGGCTT	18	1	1	3.00	3	3	0	0	0	0	0
..GTAATGTCGTCTAGGCTGA	19	1	1	2.00	2	2	0	0	0	0	0
..GTAATGTCGTCTAGGCTGCTC	21	1	1	2.00	2	0	0	2	0	0	0
..GTAATGTCGTCTAGGCTTT	19	2	2	1.50	3	3	0	0	0	0	0
..CTCACAGAGTCGAAGGACACGAA	23	0	1	1.00	1	0	1	0	0	0	0
..GTAATGTCGTCTAGGCTGCTTC	22	2	1	1.00	1	1	0	0	0	0	0
..GTAATGTCGTCTAGGCTGCG	20	1	1	1.00	1	1	0	0	0	0	0
..GTAATGTCGTCTAGG	15	0	1	1.00	1	1	0	0	0	0	0
..AATGTCGTCTAGGCTGCTA	19	0	1	1.00	1	0	1	0	0	0	0
..GCAGTCGAGACGGCACAGATG	21	0	1	1.00	1	0	0	1	0	0	0
..GTAATGTCGTCTAGGCTGCTATTA	24	2	1	1.00	1	1	0	0	0	0	0
..CAAGATGGCAGTCGAGACGG	20	0	1	1.00	1	1	0	0	0	0	0
..GTAATGTCGTCTAGGCTGG	19	1	1	1.00	1	0	0	0	1	0	0
..TCCTGCAAGATGGCAGTCGAG	21	0	1	1.00	1	0	1	0	0	0	0
..GATGGCAGTCGAGACGGCACAG	22	0	1	1.00	1	0	0	0	1	0	0
..GTAATGTCGTCTAGGCTGCTAAAA	24	3	1	1.00	1	1	0	0	0	0	0
..AGGAGTTGTCCGAGGACCTGG	21	0	1	1.00	1	1	0	0	0	0	0
..TAATGTCGTCTAGGCTGCTATC	22	0	1	1.00	1	1	0	0	0	0	0
..AGTAATGTCGTCTAGGCTGCTAA	23	1	1	1.00	1	1	0	0	0	0	0
..AATGTCGTCTAGGCTGCTATCTC	23	0	1	1.00	1	1	0	0	0	0	0
..GTAATGTCGTCTAGGCTCTA	20	3	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TAAAATTTCAAACGGTCTAGGAAACTATGTAGGAGGCCAGGACGTTCTACCGTCAGCTCTGCCGTGTCTACGGTGATAAAAGTTCCTAAGGAAATAGTGACCTTTACTACCGTCATTACAGCAGATCCGACGATAGAGTGTCTCAGCTTCCTGTGCTTCCTCAACAGGCTCCTGGACCGGTTGAA **********	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group3:7672052-7672236 +	dps_27	ATTTTAAAGTTTGCCAGATCCTTTGATACATCCTCCGGTCCTGCAAGATGGCAGTCGAGACGGCACAGATGCCACTATTTTCAAGGATTCCTTTATCACTGGAAATGATGGCAGTAATGTCGTCTAGGCTGCTATCTCACAG-AGTCGAAGGACACGAAGGAGTTGTCCGAGGACCTGGCCAACTT
droPer2	scaffold_1:9118001-9118185 +	dpe_179	ATTTTAAAGTTTGCCAGATCCTTTGATACATCCTCCGGTCCTGCAAGATGGCAGTCGAGCGGGCACAGATGCCACTATTTTCAAGGATTCCTTTATCACTGGAAATGATGGCAGTAATGTCGTCTAGGCTGCCATCTCACAG-AGTCGAAGGACACGAAGGAGTTGTCCGAGGACCTGGCCAACTT
droWil2	scf2_1100000004909:3960573-3960661 -		GATTTGAAGTTGGCCAAATGATTGGACA----------GCTCTTCCGTATCTTTGAGAGCTTGAGAGATGGGAGCGGAGACGGCATAGATGC----------GAGCATT
droVir3	scaffold_13042:3103982-3104070 +		GACTTGAAGTTGGCCAAATGATTGGACA----------GCTCCTCCGTGTCTTGGCCTCCTGCGAGATGGCCGCCGGAGACGGCATAGA----------TGCCAGCATT
droMoj3	scaffold_6328:3551629-3551728 -		AT----------TCGTTTCTGTGTGGCAACGCCGGCATCTATGCCGTCTCCGCTGCCATATCCGAGGAGAGAAAGAATACGGAGGAACTCTCCATGGACTTGGCCAACTT
droGri2	scaffold_15081:3137872-3137955 -		GACTTGAAGTTGGCCAAGTGATTCGACA----------GCTCCTCAATGTCCTTGGCCTCCTGTGAGATGGGCGCCGGACACGGCGTAGATGCGA----------
droAna3	scaffold_13417:921611-921696 -		----------GGCAATGCCGGCATCTACGCCGTATCGGCAGCCATCTCACAAGCGAACAAGGACACCCAAGAGCTGTCCAACGACCTGGCCAACTT
droBip1	scf7180000396362:271658-271753 +		AT----------TCCTT----TGCGGAAATGCCGGCATCTACGCCGTATCGGCGGCCATCTCACAGGCCAACAAAGACACCGAAGAGCTGTCCAACGACCTGGCCAACTT
droKik1	scf7180000302724:175364-175449 +		----------GGCAATGCCGGCATCTATGCCGTCTCCGGCGGCCATCTCGCAGGCTCTCAAGGACACCGAGGAGCTGTCCAACGATCTGGCCCACTT
droFic1	scf7180000453882:940306-940405 +		AC----------TCCTTCTTGTGCGGCAATGCTGGGATCTACGCCGTCTCGGCGGCCATTTCGCAGGCGGTGAAGGACACCGAGGAGCTGTCCAACGACCTGGCCAACTT
droEle1	scf7180000490214:308740-308839 -		AC----------TCCTTTCTGTGCGGCAATGCCGGGATCTATGCCGTCTCTGCGGCCATCTCACAGGCGGTCAAGGACACCGAGGAGCTGTCCAACGATCTGGCCAACTT
droRho1	scf7180000776532:323358-323443 -		----------GGCAATGCCGGCATCTATGCCGTTTCGGCAGCCATCTCGCAGGCGATCAAGGACACCGAGGAGCTGTGGAACGACCTGGCCAACTT
droBia1	scf7180000302126:3983799-3983898 +		AC----------TCCTTTCTGTGCGGCAATGCCGGCATCTATGCCGTTTCGGCGGCCATCTCGCAGGCGCTCAAGGACACCGAGGAGCTGTCCAACGATTTGGCCAACTT
droTak1	scf7180000415394:877649-877748 +		AC----------TCCTTTCTGTGCGGCAATGCCGGCATCTATGCCGTTTCGGCGGCCATCTCCCAGGAGCTCAAGGACACCGAGGAGCTGTCCAACGATTTGGCCAACTT
dm3	chrX:10987400-10987499 +		AC----------TCCTTTCTGTGCGGCAATGCTGGTATCTATGCCGTCTCGGCAGCCATATCGCAGGCGCTCAAGGAGACCGAGGAGCTTTCCGACGACTTGGCCAACTT
droSim2	x:10443526-10443625 +		AC----------TCCTTCCTGTGCGGCAATGCTGGGATCTATGCCGTCTCGGCAGCAATCTCGCAGGAGCTGAAGGACACCGAGGAGCTGTCCGATGACTTGGCCAACTT
droSec2	scaffold_15:1698456-1698555 +		AC----------TCCTTTCTGTGCGGCAATGCTGGGATCTATGCCGTCTCGGCAGCCATCTCGCAGGAGCTGAAGGACACCGAGGAGCTCTCCGATGACTTGGCCAACTT
droYak3	X:11131417-11131516 -		AC----------TCCTTCCTTGCGGCAATGCTGGAATCTATGCCGTCTCGGCAGCCATTTCGCAGGAGCTCAAGGACACCGAGGAGCTGTCCGACGACTTGGCCAACTT
droEre2	scaffold_4690:4138772-4138869 -		----------TCCTTCCTGTGCGGCAATGCTGGGATCTATGCCGTCTCTGCAGCCATTTCGCAGGAGCTCAAGGATACCGAGGAGCTGTCCGAGGACTTGGCCAACTT

Generated: 09/08/2015 at 08:15 PM

	PASS/FAIL
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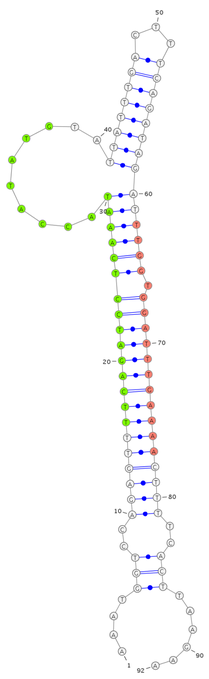
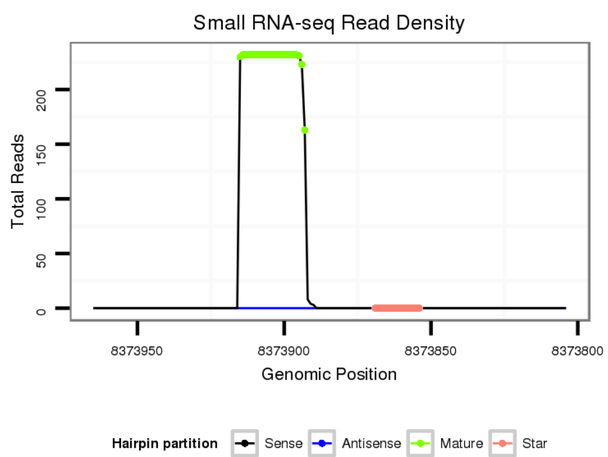
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

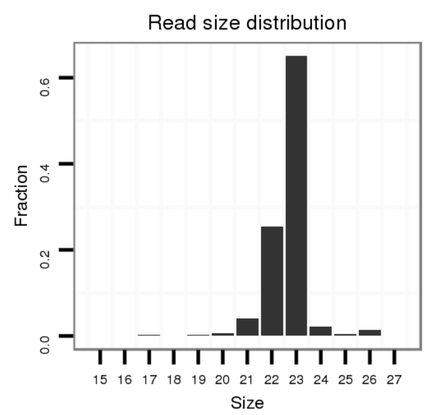
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_37	**XL_group1e:8373854-8373915 -**	**candidate-rescued**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

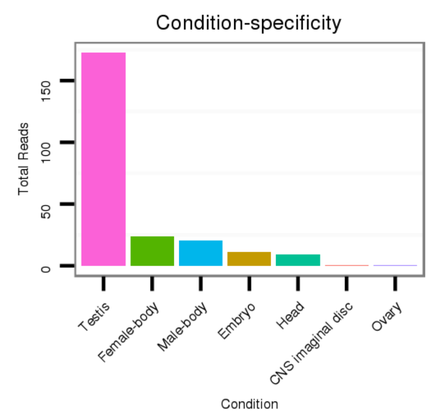
Legend: mature star mismatch in alignment mismatch in read

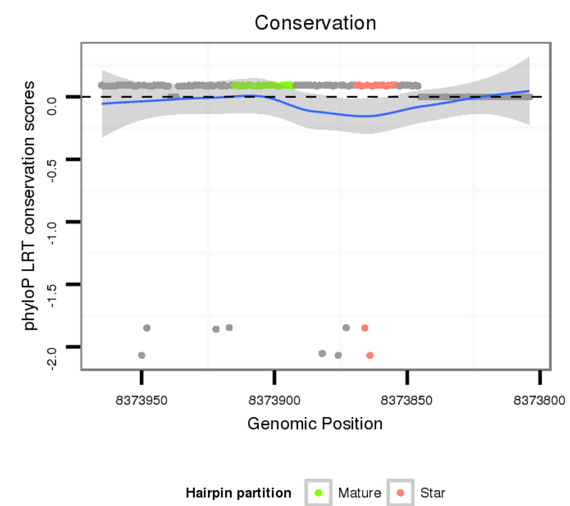
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dps_37 XL_group1e:8373893-8373915 - 2. dps-mir-2517a-2 XL_group1e:8378088-8378110 - 3. dps-mir-2517a-3 XL_group1e:8380490-8380512 - 4. dps-mir-2517a-1 Unknown_singleton_1920:1615-1637 +	1. dps_37 XL_group1e:8373854-8373869 - 2. dps_245 XL_group1e:8374602-8374617 - 3. dps-mir-2517a-2 XL_group1e:8378049-8378064 - 4. dps-mir-2517a-3 XL_group1e:8380451-8380466 - 5. dps-mir-2517a-1 Unknown_singleton_1920:1661-1676 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGGGCGAATAAACGAGTGCGAATAGCCGCCGGGTCAAATGGTCCAGAGTTTTCAGATCCTCAAATACCATATGTATTATTTGACTTTCAGATAGATTTGGTGGATTTGAAAACTTTTCACTTAAGAACACTTGATACAAGTCTCTATCTCAACGAATATTTT **********....(((..(((((((((((((((((((.....(((((((((...)))))))))))))))).))))))))))))))..)))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	V112 male body	M062 head	M059 embryo	GSM343916 embryo	M022 male body	GSM444067 head	SRR902012 CNS imaginal disc	SRR902010 ovaries
....TTCAGATCCTCAAATACCATATG	23	0	4	154.75	619	502	32	25	15	12	11	15	6	1	0
....TTCAGATCCTCAAATACCATAT	22	0	4	59.25	237	143	38	24	7	7	13	0	3	1	1
....TTCAGATCCTCAAATACCATA	21	0	4	8.25	33	16	7	4	3	1	0	1	1	0	0
....TTCAGATCCTCAAATACCATATC	23	1	4	5.50	22	15	0	5	2	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGA	24	1	4	5.00	20	19	0	1	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGT	24	0	4	4.75	19	5	3	10	0	0	0	0	1	0	0
....TTCAGATCCTCAAATACCATATGTAT	26	0	4	3.25	13	12	1	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATAA	22	1	4	2.75	11	10	0	0	1	0	0	0	0	0	0
....TTCAGATCCTCAAATACCAT	20	0	4	1.75	7	2	4	1	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATT	23	1	4	1.75	7	6	0	1	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTC	25	1	4	1.50	6	3	0	3	0	0	0	0	0	0	0
....TCAGATCCTCAAATACCATATG	22	0	4	1.50	6	1	3	0	0	2	0	0	0	0	0
....TCAGATCCTCAAATACCATAT	21	0	4	1.25	5	0	5	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATCCC	25	3	4	1.00	4	2	1	0	1	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTA	25	0	4	1.00	4	4	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTCC	26	2	4	0.75	3	1	0	2	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATCA	24	2	4	0.75	3	3	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATCC	24	2	4	0.75	3	3	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGC	24	1	4	0.50	2	1	0	0	0	1	0	0	0	0	0
....TTCAGATCCTCAAATAC	17	0	6	0.33	2	2	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTAAA	27	2	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TCAGATCCTCAAATACCATATGT	23	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATCCT	25	3	4	0.25	1	0	0	0	0	0	0	0	1	0	0
....TTTCAGATCCTCAAATACCATATG	24	0	4	0.25	1	0	0	0	0	0	0	1	0	0	0
....TCAGATCCTCAAATACCATATGTA	24	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATT	21	1	4	0.25	1	0	1	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATA	23	1	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGCCC	26	3	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTATT	27	0	4	0.25	1	0	1	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCAC	20	1	4	0.25	1	0	0	0	0	1	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTCA	26	2	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTAC	26	1	4	0.25	1	0	0	0	1	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATAG	22	1	4	0.25	1	0	0	0	0	1	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTCAA	27	3	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCATATGTG	25	1	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTCAGATCCTCAAATACCA	19	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0
....TTGGTGGATTTGAAAA	16	0	5	0.20	1	1	0	0	0	0	0	0	0	0	0
....ATTTGGTGGATTTGAAA	17	0	5	0.20	1	1	0	0	0	0	0	0	0	0	0
....GATTTGGTGGATTTGAAA	18	0	5	0.20	1	0	0	1	0	0	0	0	0	0	0
....GATTTGGTGGATTTGAAAA	19	0	5	0.20	1	0	0	1	0	0	0	0	0	0	0
....TTTGGTGGATTTGAAA	16	0	6	0.17	1	1	0	0	0	0	0	0	0	0	0
....TTGGTGGATTTGAAA	15	0	8	0.13	1	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACCCGCTTATTTGCTCACGCTTATCGGCGGCCCAGTTTACCAGGTCTCAAAAGTCTAGGAGTTTATGGTATACATAATAAACTGAAAGTCTATCTAAACCACCTAAACTTTTGAAAAGTGAATTCTTGTGAACTATGTTCAGAGATAGAGTTGCTTATAAAA **********....(((..(((((((((((((((((((.....(((((((((...)))))))))))))))).))))))))))))))..)))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	M040 female body	M059 embryo	SRR902012 CNS imaginal disc	GSM343916 embryo
....TACCAGGTCTCAAAAGTCTAGGA	23	0	6	0.50	3	3	0	0	0	0
....AAGTCTAGGAGTTTATGGTATACAT	25	0	4	0.25	1	0	0	1	0	0
....CGGCGGCCCAGTTTACCAGGTCTCAAA	27	0	4	0.25	1	0	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group1e:8373804-8373965 -	dps_37	TGGGCGAATAAACGAGTGCGAATAGCCGCCGGGTCAAATGGTCCAGAGTTTTCAGATCCTCAAATACCATATGTATTATTTGACTTTCAGATAGATTTGGTGGATTTGAAAACTTTTCACTTAAGAACACTTGATACAAGTCTCTATCTCAACGAATATTTT
droPer2	scaffold_13:188241-188357 +		TGGGCGAATAAACGATTACGAATAGC---CGGGTCAAATGGTCTAGAGCTTTCAGATCCTCAAATACCATATGTATTATTTGAATTTCATATGGATTTGATTGATTTGAAAACTTTTCAG----------

Generated: 09/08/2015 at 08:44 PM

	PASS/FAIL
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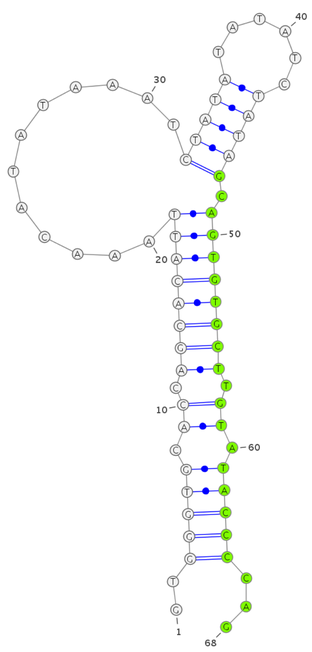
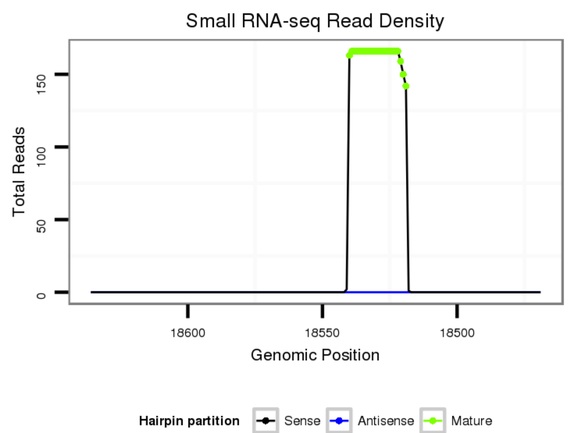
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	1

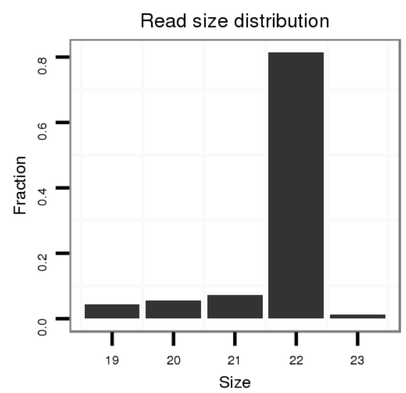
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_2346	**Unknown_singleton_294:18519-18586 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

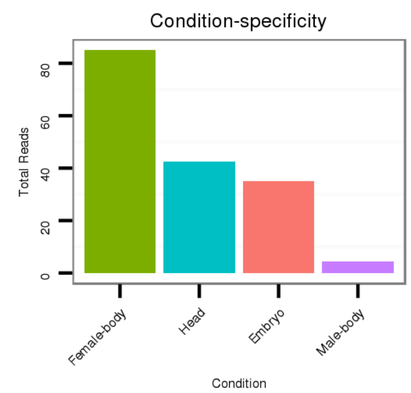
Legend: mature star mismatch in alignment mismatch in read

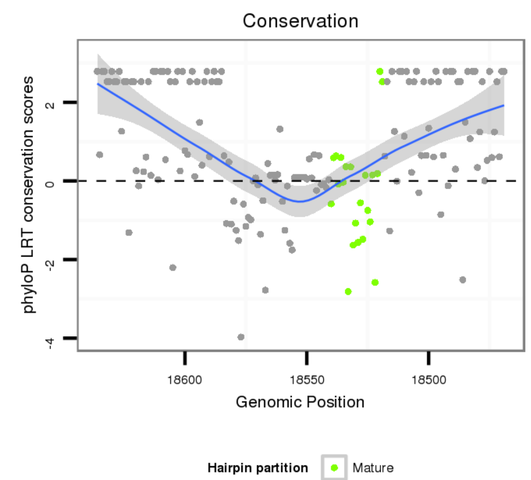
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA22194-in]; CDS [Dpse\GA22194-cds]; CDS [Dpse\GA22194-cds]

No Repeatable elements found

mature	star
1. dps_455 2:10181426-10181447 + 2. dps_2346 Unknown_singleton_294:18519-18540 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTCCAGGAAGAGCAGGTGGGTGCACCAGCACATTAAACATATAAATCTATATATATCTATAGCAGTGTGCTTGTATACCCCAGACAACCAAGACACAGTCGTCCACTCTGATCCCCATCAATCGATTGACCAT **********..(((((.((.((((((((.....((((.....)))))).)))))))).)).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M059 embryo	GSM343916 embryo	M062 head	V112 male body
.....GCAGTGTGCTTGTATACCCCAG.....	22	0	2	136.00	272	131	45	33	33	22	8
.....GCAGTGTGCTTGTATACCCC.....	20	0	2	9.00	18	12	2	1	0	2	1
.....GCAGTGTGCTTGTATACCCCA.....	21	0	2	8.50	17	12	1	3	0	1	0
.....GCAGTGTGCTTGTATACCC.....	19	0	2	7.00	14	4	4	0	0	6	0
.....GCAGTGTGCTTGTATACCCCAGT.....	23	1	2	5.00	10	5	1	2	1	1	0
.....CAGTGTGCTTGTATACCCCAG.....	21	0	2	3.50	7	7	0	0	0	0	0
.....AGCAGTGTGCTTGTATACCCCAG.....	23	0	2	2.00	4	2	2	0	0	0	0
.....CAGTGTGCTTGTATACCCCAGT.....	22	1	2	1.50	3	1	0	1	0	1	0
.....GCAGTGTGCTTGTATACCCCAC.....	22	1	2	1.50	3	0	0	3	0	0	0
.....GCAGTGTGCTTGTATACCCCAGC.....	23	1	2	1.00	2	1	0	0	1	0	0
.....GCAGTGTGCTTGTATACCCCAGA.....	23	0	2	1.00	2	2	0	0	0	0	0
.....AGTGTGCTTGTATACCCCAG.....	20	0	2	0.50	1	1	0	0	0	0	0
.....CAATTACACTCAGTTCCAGGAAGAGCAG.....	28	0	2	0.50	1	1	0	0	0	0	0
.....CAGTGTGCTTGTATACCCCAGC.....	22	1	2	0.50	1	0	0	0	0	1	0
.....GCAGTGTGCTTGTATACCCCAT.....	22	1	2	0.50	1	0	1	0	0	0	0
.....GCAGTGTGCTTGTATACCCCAGTA.....	24	2	2	0.50	1	1	0	0	0	0	0
.....CAGTGTGCTTGTATACCCC.....	19	0	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

ACTTCCAGCTCGCACGGTCCGCGTTAATGTGAGTCAAGGTCCTTCTCGTCCACCCACGTGGTCGTGTAATTTGTATATTTAGATATATATAGATATCGTCACACGAACATATGGGGTCTGTTGGTTCTGTGTCAGCAGGTGAGACTAGGGGTAGTTAGCTAACTGGTA **********..(((((.((.((((((((.....((((.....)))))).)))))))).)).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	Unknown_singleton_294:18469-18636 -	dps_2346	TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTCCAG-GAAGAGCAGGTGGGTGCACC--A-GCA-----CA--TTAAA----CATATAAATCTATA-----TATATC----------T------ATAGC--A----G----------TGT-GCTTGTA--TAC----CCCAGACAACCAAGACACAGTCGTCCACT-CTGATCCCCATCAATCGATTGACCAT
droPer2	scaffold_0:10300282-10300453 -	dpe_462	TGAAGGTCGAGCGTGCCAGGCGCAATTACACGCAGTTCCAG-GAAGAGCAGGTGGGTGCACC--A-GCA-----CA--TTAAACATA----TAAAGCTATATAT-GTATATC----------T------ATAGC--A----G----------TGT-GCTTGTA--TAC----CCCAGACAACCAAGACACAGTCGTCCACT-CTGATCCCGATCAATCGATTGCCCAT
droWil2	scf2_1100000004902:9022539-9022701 -		TGAAGGTCGAACGAGCTAGACGTAATTATACACAATTCCAA-GAGGAACAGGTACCA-----------------CACACATATCAAG-----AATT-----GTTTTGTACTCAA--------TGTAA----CAC--A----AAT----------ACTTTTC--TTT----TGTAGCGCACCAAAACTCAGTCGTCCAGA-CTTATTCCAATCAATCGTTTGCCCAT
droVir3	scaffold_12822:3790401-3790564 -		TGAAGGTCGAGCGTGCCAGGCGCAATTATACCAGTTTCAG-GAGGAGCAGGTGGGTGCAGT--T-T---------A----AATCA----A----------AATTG---AAAA--GTCTCTG----AG----------GTAA-----------TGATATAT-----AGTA--TC-ATCTA-TTG----TCTAGCCAATTAAAACACAAGCGCAACA-CTAATACCTATTAATCGTTTGCCCAT
droMoj3	scaffold_6540:17099574-17099735 -		TGAAGGTCGAGCGTGCCAGGCGCAATTATACGCAATACCAA-GAGGAGCAGGTGGGTGCACT--TAGCA-----AA--TCAAA----------AGTGTGCTGG----AG----------GTAA-----TGCCGA----CAT----------CCGGTCC--AAT----TTTAGCGCACCAAAACACAGACGGCCACC-CTCATACCCATTAATCGTTTGCCCAT
droGri2	scaffold_14906:1382895-1383059 -		TGAAGGTCGAGCGGCCCGGCGCAACTATACACAGTACCAA-GAGGAGCAGGTGTGTACAGT--C-GGC-----TATA----AATCA----A----------GATTG-----ATGTCCTTG----AA----------GTAA-----TAC--A----ATT----------G-CGGTCC--AAT----TTCAGCAACTAAAACACAAGCAGCCACA-CTCATACCTATCAATCGCGTGCCCAT
droAna3	scaffold_13340:17149374-17149541 -		TGAAGGTCGAGCGCGCTCGAAGGAACTACACCGCAGTTCCAA-GAAGAACAGGTAGGAGTCGC-TA-CCC-----CA--ACAGG----TTCAGAAAC------AT-ACTT----------GG----------TG-----AACAGT--A----ATG----------A-CGTTTATTTT----GCACGGCTACAAAGACACAGTCGTCCACT-TTGATACCCATCAATCGACTGCCCAT
droBip1	scf7180000396424:652032-652199 -		TGAAGGTCGAGCGCGCTCGAAGGAACTACACCGCAGTTCCAA-GAAGAGCAGGTAGGAGTCAC-TG-GCG-----CA--CCCAC----TTCACAATC------AT-GGTTACC----------T-----AACAGT--A----ATG----------A-CGTTTATTTT----GCCAGGCCACAAAGACACAGTCGTCCACC-TTGATACCCATCAATCGACTGCCTAT
droKik1	scf7180000302256:110322-110486 -		TGAAGGTCGAGCGCGCTCGGCGCGAATTACACCGAGTTCCAG-GAAGAGCAGGTGACTTAACC--T---------ACA----GTCCT----C-TT-------AGAT-----GGTCCGTTCAAAT----------CGCA-----AT--A----AAC----------CCTTCTCCATTT----TACAGGCCACCAAGACACAGTCGTCCACC-CTGATACCGATCAACCGACTTCCCAT
droFic1	scf7180000453581:272813-272965 +		TGAAGGTCGAGCGTGCCAGGAGCGAATTACACCAGTTTCAG-GAGGAGCAGGTGGGCTTAGC--T-T---------GCA----ATA----------GG----------TGTATCTGACTATT--A----T----------ATCTATTTTTGTAGACACTCCACCAAGACACAATCGTCCACT-TTGATACCGATCAACCGACTTCCCAT
droEle1	scf7180000491280:3591270-3591445 +		TGAAGGTCGAGCGACCCGCCGGAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGGTTCTACTTTGGTACTAGT--ACTAC----TTTAC--C-------AA----------TAAAT-----CAGTGGTATATAACAGCGTTT-CCT--TA--ATG----CACAGGCCACCAAGACGCAATCGTCAAGC-CTGATTCCAATCAATCGACTTCCCAT
droRho1	scf7180000779501:61345-61505 -		TGAAGGTCGAGCGACCCGGCGCAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGCATGGG--T---------GTA----CAC-C----C-TG-------GG----------CCAGT-----CACTTATA----ACAGAATAC-CTCTCCC--AAC----GCAGGCCACCAAGACGCAGTCGTCCACT-CTGATACCCATCAATCGACTTCCCAT
droBia1	scf7180000302075:2440004-2440169 +		TGAAGGTCGAGCGTGCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGGGCCACCT--T---------G----G--------GGTCTACTCAATTCAAT-----TGATTATCTATGACAGACTAT-ACCTCTC--ATC----GCCAGGCCACCAAGACGCAATCGTCCACT-CTGATACCGATCAATCGACTTCCAAT
droTak1	scf7180000415383:115705-115865 +		TGAAGGTCGAGCGTGCCAGGCGCAATTACACTCAGTTTCAG-GAGGAGCAGGTGGGTTGTTG--T-CTC-----CA--CTTAA----T----------ACAAC-----AAGATATCTAT-----AATATATAACCTA-TTA----GATAGCCACCAAGACGCAATCGTCCACT-CTGATACCGATCAATCGACTTCCCAT
droEug1	scf7180000409787:1235183-1235345 +		TGAAGGTCGAGCGTGCCCGGCGCAATTATACTCAATTTCAG-GAGGAGCAGGTGGGTTTTTG--G-T-----TT----ACTCA----ATAC------CG----------CCGA-----------TTATTTATAACATCCCAT-CCTTTGT--ACC----AACAGGCCACCAAGACGCAATCGTCCACT-CTTATACCAATCAATAGATTCCCAT
dm3	chr3R:24345661-24345822 -		TGAAGGTCGAGCGGCCCGGCGCAACTACACTCAGTTTCAG-GGGAGCAGGTGGGTTAAGG--T---------ACA----ACCCA----CAAC------GG----------TCAAT-----ATGTTATATAT-----AGTAT-GCAACCT--ACT----GCAGGCTACCAAGACGCAGTCGTCCACT-CTGATACCAATCAACCGTCTACCCAT
droSim2	3r:23723760-23723921 -		TGAAGGTCGAGCGCGCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGAGTAGAGG--T---------ACA----ACCCA----CAAC------GG----------TCAAT-----ATGTTATATAT-----AGTAT-CCAACCT--ACT----GCAGGCCACCAAGACGCAGTCGTCCACT-CTGATACCAATCAACCGTCTACCCAT
droSec2	scaffold_22:948938-949100 -		TAAAGGTCGAGCGCGCCCGGCGCAACTACACTCAGTTTCAGGGAGCAGGTGGGTAGTACAGG--T---------ACA----ACCCA----C-AC------GG----------TCAAT-----ATGTTATATAT-----AGTAT-CCAACCT--ACT----GCAGGCTACTAAGACGCAGTCGTCCACTCTGATACCATTCAACCGTCTACCCAT
droYak3	3R:22151663-22151827 +		TGAAGGTCGAGCGCGCCCGGCGCAACTACACTCAGTTTCAG-GAGGAGCAGGTGCGCTAACC--C---------ACATCC-ACCCA----CTAC------GG----------TCAAT-----ATGTTATATAG-----AGTAT-CTTATCC--AAT----GCAGGCCACCAAGACGCAGTCATCCACC-CTGATACCGATCAACCGACTACCCAT
droEre2	scaffold_4820:3689926-3690090 +		TAAAGGTCGAGCGCGCCCGGCGCAACTACACCCAGTTTCAG-GAGGAGCAGGTGCGCTAG---T-CC-----CACTT-AAACCCT----CCTT------GG----------TCAAT-----ATGCTATATAT-----AGTAT-CCTAACT--AAT----GCAGGCCACCAAGACACAGTCGTCCACT-CTGATACCGATCAACCGACTACCCAT

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rescue.confident	1
rescue.candidate	2

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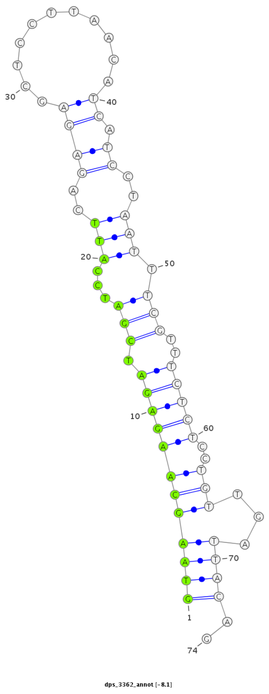
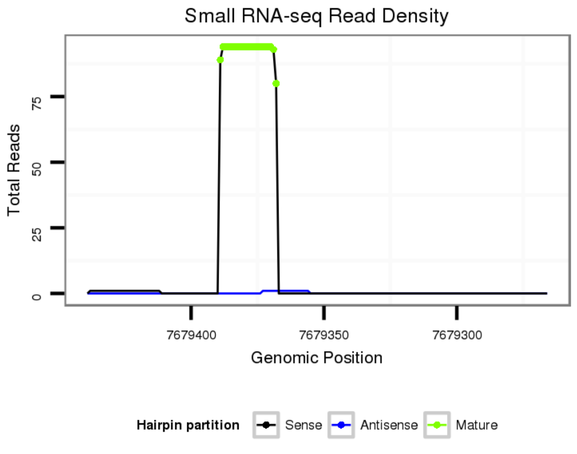
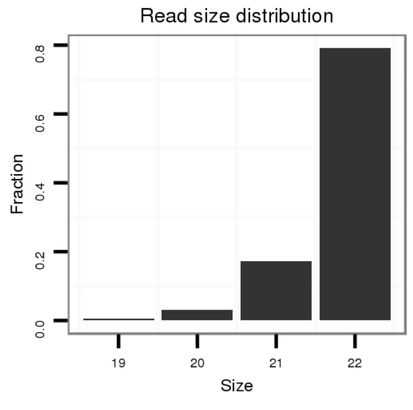
dps_3362	**XR_group8:7679316-7679389 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

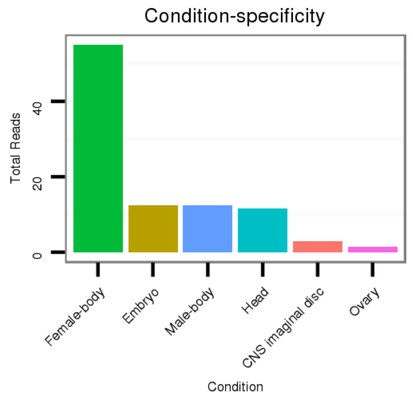
Legend: mature star mismatch in alignment mismatch in read

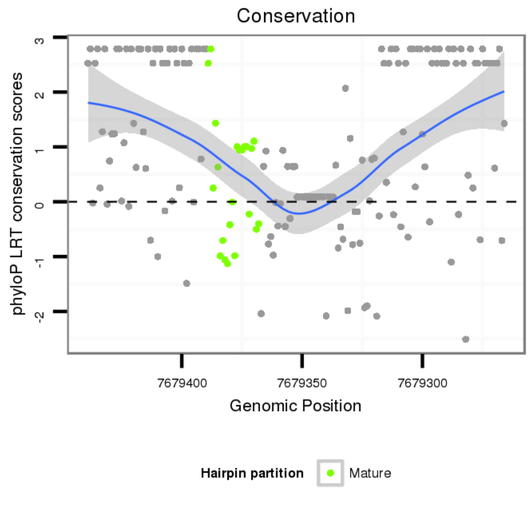
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GA21329-in]; CDS [Dpse\GA21329-cds]; CDS [Dpse\GA21329-cds]

No Repeatable elements found

mature	star
1. dps-mir-2572 2:11390-11411 + 2. dps_3362 XR_group8:7679368-7679389 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGGAACTGGCCAAACTGAACTTCCTGGAGAGTCATAGCTCTGAATTTAAGTAAGCAAGAGATCGATCCATTCAGAGAGCTCCTTAACATCATCCTAATTTCGTTTCTCTCCTGTTGATTACAGTGTAACCCGCAACTACCTCGACTGGCTCACCTCGCTACCCTGGGGCGTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	V112 male body	GSM444067 head	GSM343916 embryo	M062 head	SRR902012 CNS imaginal disc	SRR902010 ovaries
**********(((((((((((.(((...(((..((((...........)).)).)..))).))))..))))))..))))...))))).**********													
.....GTAAGCAAGAGATCGATCCATT.....	22	0	2	76.00	152	85	13	19	14	6	7	6	2
.....GTAAGCAAGAGATCGATCCAT.....	21	0	2	12.50	25	15	1	4	0	3	1	0	1
.....TAAGCAAGAGATCGATCCATT.....	21	0	2	4.00	8	6	1	0	1	0	0	0	0
.....GTAAGCAAGAGATCGATCCA.....	20	0	2	1.50	3	2	0	1	0	0	0	0	0
.....GTAAGCAAGAGATCGATCCATC.....	22	1	2	1.50	3	0	2	0	0	0	1	0	0
.AGGAACTGGCCAAACTGAACTTCCTGG.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TAAGCAAGAGATCGATCCAT.....	20	0	2	1.00	2	0	1	1	0	0	0	0	0
.....GTAAGCAAGAGATCGATCC.....	19	0	2	0.50	1	1	0	0	0	0	0	0	0
.....GTAAGCAAGAGATCGATCCATTT.....	23	1	2	0.50	1	1	0	0	0	0	0	0	0
.....CGCAACTACCTCGACTGGCTCACCTCGCT.....	29	0	2	0.50	1	1	0	0	0	0	0	0	0
.....CTGAACTTCCTGGAGAGTCA.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0
.....AAGCAAGAGATCGATCCATT.....	20	0	2	0.50	1	1	0	0	0	0	0	0	0
.....AACTGAACTTCCTGGAGAGTC.....	21	0	2	0.50	1	1	0	0	0	0	0	0	0
.....CCTCGCTACCCTGGGGCGTCA	21	0	3	0.33	1	1	0	0	0	0	0	0	0
.....GTAAGCAAGAGATCGATTTT.....	20	3	7	0.14	1	0	0	0	1	0	0	0	0

Anti-sense strand reads

CTCCTTGACCGGTTTGACTTGAAGGACCTCTCAGTATCGAGACTTAAATTCATTCGTTCTCTAGCTAGGTAAGTCTCTCGAGGAATTGTAGTAGGATTAAAGCAAAGAGAGGACAACTAATGTCACATTGGGCGTTGATGGAGCTGACCGAGTGGAGCGATGGGACCCCGCAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902011 testis	V112 male body
**********(((((((((((.(((...(((..((((...........)).)).)..))).))))..))))))..))))...))))).**********							
.....AGGTAAGTCTCTCGAGGA.....	18	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XR_group8:7679266-7679439 -	dps_3362	GAGGAACTGGCCAAACTGAACTTCCTGGAGAGTCATAGCTCTGAATTTAAGTAAGCAA----GAGATCGATCC----------AT-TCAGAG--AGC-TCCTTAACATCATCCTAATTTCG-----TTTC-------TC---------TCCTGTTGATTACAGTGTAACCCGCAACTACCTCGACTGGCTCACCTCGCTACCCTGGGGCGTCA
droPer2	scaffold_48:457716-457889 -	dpe_1725	GAGGAACTGACCAAACTGAACTTCCTGGAGAGTCATAGCTCTGAATTTAAGTAAGCAA----GAGATCGATCC----------AT-TCAGAG--AGC-TCCTTAACATCATCCTAATGTCG-----TTTC-------TC---------TCCTGTTAATTACAGTGTAACCCGCAACTACCTCGACTGGCTCACCTCGCTACCCTGGGGCGTCA
droWil2	scf2_1100000004540:869876-870033 +		GAAGAGCTGACCAAACTCAATTTCCTTGAGAGCCACAGCTCAGAGTTTAAGTAAGTGTCTGCAAGCTCGATTC----CTCC--------TGC--CG----------ACT----CCCGT-----------------------CTAAT-----------------CTCTATTTTGCAGTGTCACACGCAACTACCTCGACTGGCTGACCTCTTTGCCATGGGGCGTAA
droVir3	scaffold_13049:13184480-13184636 -		GAAGAGCTGACCAAGTTAAATTTCTTGGAAAGTCACAGCTCGGAATTTAAGTGAGTCGC---CAG------CTTTAAAA-------TGT-TAA-------TACAT-------A-T-----------------------TTCATTAAT-T---------TGTC-TCTATTGTAGTGTTACACGAAACTATTTAGACTGGCTCACCTCATTGCCTTGGGGCGTCA
droMoj3	scaffold_6680:14177853-14178018 +		GAAGAGCTCACCAAGTTGAACTTCTTGGAGAGTCACAGCTCAGAGTTTAAGTGAGTCCCTCTCT-C-------------TCTCTCTCTCTCTCTG----------AAG--C-TCTGT-----------------------GTAA-TAATATA---------TCCTATTCTTTGTAGTGTTACTCGCAACTATCTGGACTGGCTTACCTCTTTGCCTTGGGGCGTCA
droGri2	scaffold_15110:18623605-18623765 -		GAGGAACTGACCAAGCTGAACTTCTTAGAAAGTCACAGTTCGGAATTCAAGTGAGTCGT---CAGTCGAT--------TA---------TTATT------CAT----T----TGTCGAAC-----------------------CTCAACAA--TA---------TGGTTTTATTCTAGCGTTACACGAAATTATTTAGACTGGCTCACCTCATTGCCTTGGGGCGTTA
droAna3	scaffold_13337:17286842-17287000 +		GAAGAGCTGACCAAGCTGAACTTCCTGGAGAGCCATAGTTCGGAGTTTAAGTAAGTATATCT------------TGGAAA--------ACC-TTA-------TAAAG----GC---T-----------------------TCTATTGAT----CGTATTA---T-CTAATTTTAGTGTCACCCGCAACTACCTCGACTGGCTGACCTCGCTGCCATGGGGCGTCA
droBip1	scf7180000396741:583178-583336 +		GAAGAGCTGAATAAGCTAAGCTTCCTTGAAAGTCATAGTTCGGAATTTAAGTATTGATA---------------GTTTTAGAG--------CCT-CTT-------TAAAT----GA----T-----------------------TCTATTAAT----CAAA---TAAT-TCCATTTTAGTGTAACTCGAAACTACCTGGACTGGCTTACCTCGCTGCCATGGGGCGTCC
droKik1	scf7180000302694:137355-137515 -		GAGGAGCTGGCCAAGCTAAACTTCCTGGAGAGTCACAGCTCTGAGTTCAAGTGAGTATTA-AGAA-------------CG---------TTCTG----------AAAAGACTTAGT-TCATAAA----------AAAC-----TA---------TCCTTTAATACGTAGTGTAACCCGCAACTACCTCGACTGGCTCACATCCCTGCCCTGGGGAGTGA
droFic1	scf7180000453831:157478-157637 -		GAAGAGCTGACCAAACTGAACTTCCTGGAGAGCCACAGCTCTGAGTTTAAGTAAGAACCTCTAA-T-------------TA---------ATTAG----------GTT----TTA-G-----------------------TATCTTATAACTTATA--------TCCCTTTGCTCTAGCGTTACCCGCAATTACCTCGACTGGCTTACCTCTCTGCCCTGGGGCGTTA
droEle1	scf7180000491249:6906338-6906493 -		GAAGAGCTGACCAAACTGAACTTCCTGGAAAGCCACAGCTCAGAGTTTAAGTAAGCCTTGCTAT-A-------------TC---------ACATA----------TAG----TTCAT-----------------------AATAACTAATATA---------TACGTCGATTCCAGTGTAACCCGCAACTACCTCGACTGGCTAACATCCCTTCCGTGGGGCGTTA
droRho1	scf7180000779964:53059-53215 -		GAAGAGCTGACCAAACTGAACTTCCTGGAAAGCCACAGCTCTGAGTTTAAGTAAGGGCTTCTAT-A-------------GT---------ACATG----------AAT----TTCGT-----------------------ACAACTAATATC---------TCCTATAATTCGTAGTGTAACCCGCAACTACCTCGACTGGCTCACTTGCCTTCCATGGGGCGTTA
droBia1	scf7180000302377:2005575-2005731 +		GAGGAGCTGACCAAACTGAACTTCCTTGAAAGCCACAGCTCTGAGTTTAAGTAAGGTCTTCTTT-T-------------CC---------GCGTG----------AAT----TTCGC-----------------------ATCACTAGCATC---------CCCTTTAATTTCCAGTGTAACCCGCAATTACCTCGACTGGCTCACTTCTTTGCCTTGGGGAGTTA
droTak1	scf7180000415276:125207-125370 -		GAGGAGCTGACCAAACTGAACTTTCTGGAGAGCCACAGCTCGGAGTTTAAGTAAAATCCGCTAT-A-------------CC---------GCATATCACATCAT----T---A----TCAGC-----------------------TACCTTAATATG---------TCCTCTAATTTGCAGTGTTACCCGCAATTACCTTGACTGGCTCACCTCATTGCCTTGGGGCGTCA
droEug1	scf7180000409472:151090-151246 -		GAAGAGTTAACCAAACTGAACTTCCTCGAAAGTCATAGCTCTGAGTTTAAGTAATAATTGTATAT-T-------------AC---------ACATG----------T-TA----TATAG-----------------------AAAACTAATATC---------TCCATACATTTTCAGCGTAACCCGTAATTACCTTGACTGGCTCACCTCTCTGCCTTGGGGCGTTA
dm3	chr3L:19603239-19603401 -		GAAGAACTCACCAAGCTGAACTTCCTGGAGAGTCATAGTTCGGAGTTTAAGTGAGTTCTACAAA-A-------------TA---------TTTTG-----G-----AAT----TTAGC-----------------------TTAACTAATATGCTCATACTA---C-TTTTTTTTAGTGTAACTCGCAATTACCTCGACTGGCTTACTTGCCTACCTTGGGGCGTTA
droSim2	3L:19253812-19253973 -	dsi_862	GAAGAGCTCACCAAGCTGAACTTCTTGGAGAGTCACAGTTCGGAGTTTAAGTGAGTTCTACTGA-A-------------TA---------CTTTG----------AAT----TTAGC-----------------------TAAACTTATATGCTCCTACTA---C-TTTTTTTTAGTGTAACTCGCAATTACCTCGACTGGCTTACTTCCCTACCTTGGGGCGTCA
droSec2	scaffold_29:306813-306974 -		GAAGAGCTCACCAAGCTGAACTTCTTGGAGAGTCACAGTTCGGAGTTTAAGTGAGTTCTACTAA-A-------------TT---------ATTTG----------AAT----TTAGC-----------------------TTAACTTATATGCTCCTACTA---C-TTTTTTTTAGTGTAACTCGCAATTACCTCGACTGGCTTACTTCGCTACCTTGGGGCGTCA
droYak3	3L:20940592-20940748 +		GAAGAGCTCACCAAGCTGAACTTCCTAGAAAGTCACAGCTCCGAGTTTAAGTGAGTATTTTTA-A-------------TA---------TTTTG----------AAT----TTAGC-----------------------TTTCCTTATATG---------TTTCTTTATTTTAGTGTAACAAGAAATTACCTCGACTGGCTTACTTGCCTACCTTGGGGCGTTA
droEre2	scaffold_4784:19401752-19401907 -		GAAGAGCTTACCAAGCTGAACTTCCTGGAGAGTCACAGCTCCGAGTTTAAGTGAGTACTTCTAA-A-------------TA---------CTTTG----------AAA----ATAGC-----------------------TTAATTAAT-TG---------TTCCTTTATTTTAGTGTAACACGTAATTACCTCGACTGGCTTACTTCCCTACCTTGGGGCGTTA

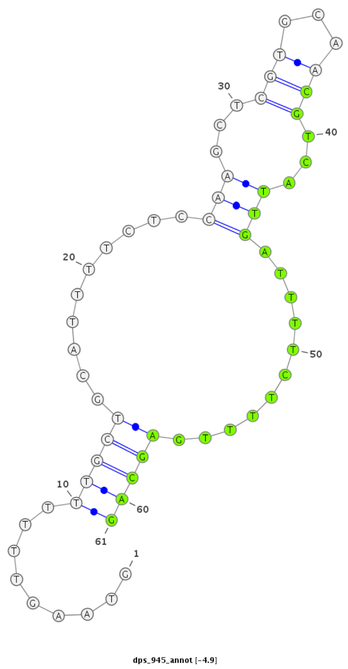
Generated: 09/08/2015 at 07:08 PM

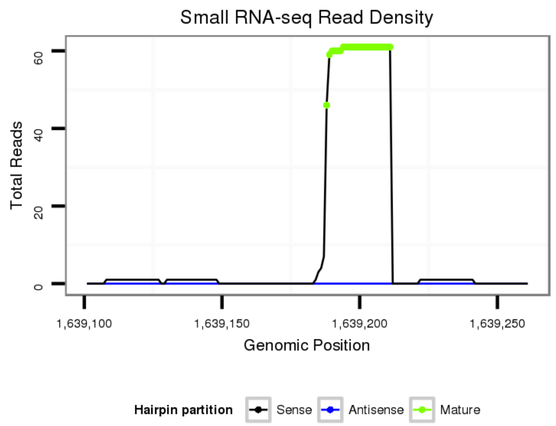
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

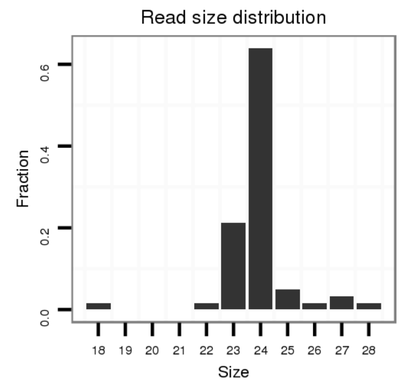
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_945	**3:1639151-1639211 +**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

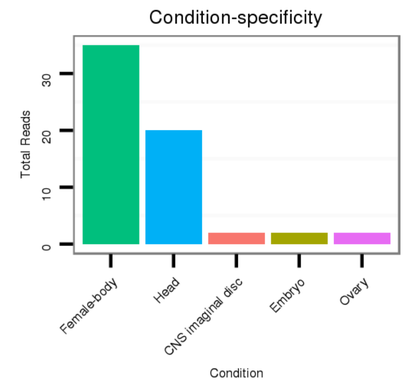
Legend: mature star mismatch in alignment mismatch in read

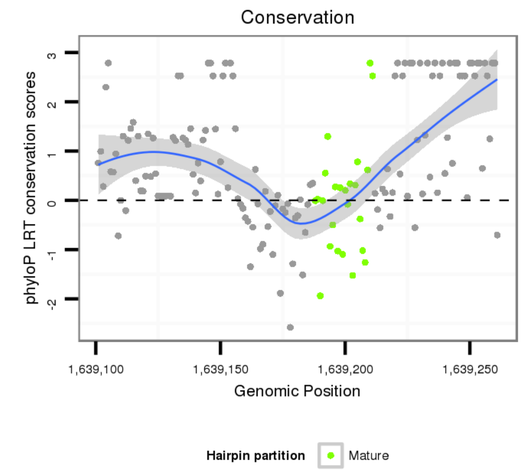
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\fak-in]; CDS [Dpse\fak-cds]; CDS [Dpse\fak-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCCAGCGTCAACCAAAGCCATCATGCGACGCCGCCCACCAGCAATGAGCGTAAGTTTTTTGCTGCATTTTCTCCAAGCTCGTGCAACGTCATTGATTTTCTTTTGAGCAGCTGTCTGCGAGGACTACGTTCTTCATGTGCATATGCCGAACAAAAGTTTC **********.....(((((.....(((...(((...)))...))).....)))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	M062 head	M059 embryo	SRR902010 ovaries	SRR902012 CNS imaginal disc	V112 male body
.....CGTCATTGATTTTCTTTTGAGCAG.....	24	0	1	39.00	39	22	13	0	1	2	1	0
.....GTCATTGATTTTCTTTTGAGCAG.....	23	0	1	13.00	13	8	5	0	0	0	0	0
.....ACGTCATTGATTTTCTTTTGAGCAG.....	25	0	1	3.00	3	3	0	0	0	0	0	0
.....CAACGTCATTGATTTTCTTTTGAGCAG.....	27	0	1	2.00	2	0	1	0	0	0	1	0
.....TCATTGATTTTCTTTTGAGCAG.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....CGCCGCCCACCAGCAATGA.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....GGACTACGTTCTTCATGTGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....GTCAACCAAAGCCATCATGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TGATTTTCTTTTGAGCAG.....	18	0	1	1.00	1	0	0	1	0	0	0	0
.....GCAACGTCATTGATTTTCTTTTGAGCAG.....	28	0	1	1.00	1	0	0	0	1	0	0	0
.....AACGTCATTGATTTTCTTTTGAGCAG.....	26	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

TCGGTCGCAGTTGGTTTCGGTAGTACGCTGCGGCGGGTGGTCGTTACTCGCATTCAAAAAACGACGTAAAAGAGGTTCGAGCACGTTGCAGTAACTAAAAGAAAACTCGTCGACAGACGCTCCTGATGCAAGAAGTACACGTATACGGCTTGTTTTCAAAG **********.....(((((.....(((...(((...)))...))).....)))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:1639101-1639261 +	dps_945	AGCCAGCGTC----------AACCAAAGC---CATCATGCGACGCCGCCCACCAGCAATGAGCGTAAGTTTT------TTG-CT-GCATTT-----TCTCC----------AA---------GCTC--G-----TG---CAA--CGTCAT-T---GAT-----T---TTCT--TTTG-----AGCAGCTGTCTGCGAGGACTACGTTCTTCATGTGCATATGCCGAACAAAAGTTTC
droPer2	scaffold_2:1816101-1816261 +	dpe_1020	AGCCAGCGTC----------AACCAAAGC---CATCATGCGACGCCGCCCACCAGCAATGAGCGTAAGTTTT------TTG-CT-GCATTT-----TCTCC----------AA---------GCTC--G-----TG---CAA--CGTCAT-T---GAT-----T---TTCT--TTTG-----AGCAGCTGTCTGCGAGGACTACGTTCTTCATGTGCATATGCCGAACAAAAGTTTC
droWil2	scf2_1100000004514:1283679-1283849 -		GGCCAGTGCTGCCGCCAACCAGAGCCAAAGTAATCAGTT------GAGGTGTTCCTGCAATGAATGTGAGAGTT------CAT-TT-GGTTAT-----TTAT-----------**--**---------**--**TT--ATTATTAT---CAA--TTGTAT-T---AAC-----TTT-C-TA--TGAT-----TTCAGTGCAATCGGAGGACTATGTACTCCATGTACATATGCCAAACAAGAGTTTT
droVir3	scaffold_12875:11833059-11833208 +		AGTCAAC---------------CAA---AGCGATCA------GCCGCATAGGAACAATGGATGTAAGTACA------TAT-AT-GGCTGC-----AAAGC-----------**--**-------CAAATT--G-----GT---TAA--TTAA-T-G---CACT-----TTT-TGTT--ATTT-----ATTAGCCAATATGAGAGTTACGTTCTTCATGTACACATGCCAAACAAGAGTTTT
droMoj3	scaffold_6496:15028016-15028174 -		GCGCAAG---------------AACCAAAGCAGT---CA------GCCGCATAAGAACAATGAATGTAAGTAAA------TAT-TGAAT----AA-TGAATGT-----------**--**----AAACATAAA--A-----TA---TAA--CATAAT-A---TAAT----TTT-ATT--GTTT-----ATTAGCCACTCTGAAGATTATGTTCTTCAGGTACATATGCCAAACAAGAGTTTT
droGri2	scaffold_15245:11681558-11681718 +		AGGCAAC---------------CAA---AGCAATCA------GCCGCATAAGAGCAATGAGTGTAAGTAAT------TT--**--**GG----AT-CAACTTT-----------**GG--**AACATTTTTA--AT----**--**---TGT--CTAA-T-A---AATTTGCAC---T-AATTTTGAAAATCTTAGCCCATTCGGAAGATTATGTGCTCCATGTGCATATGCCCAACAAGAGTTTC
droAna3	scaffold_13266:1940695-1940860 +		A---AGC---------------**--------**AGTCAAC------GCCGCCCACCAGCCATGACTGTGAGTAGGAGTTCTGGT-TT-GG----CCTCTCCAATTTTCAGATTTTCCCC--AA---------**---**A--A-----AA---ACA--CCCACT-GATT-CA-----TTG-ATCT--CTTC-----TGCAGCGCTCCTCGACGAGTACGTCATCCATGTGCACATGCCCAACAAGAGCTTC
droBip1	scf7180000396730:2926943-2927108 +		A---AGC---------------**--------**AGTCAAC------GCCGCCCACCAGCCATGACTGTGAGTAGGAGTTCTGGT-TT-GA----GCTGTCCAATTTCCAGATTTTCCCC--GA---------**---**A--A-----AA---AAA--CCCCTT-GATT-AA-----TTG-ATCT--CTTC-----TGCAGCGCTCCTCGACGAGTACGTCATCCATGTGCACATGCCCAACAAGAGCTTC
droKik1	scf7180000302471:1581974-1582135 -		AGCCAGCGCC----------AGCCACAACAGTCTACC------GCCGCCCACCCAAAATGAGATGTGAGTGTC------AGA-AT-GGGAGC-----TT-TG----------AG---------TCTC--G-----TGAGATAA--CTCAA-G---AAT-----TCTGTCTT--CTTC-----CCCAGTGTCCCTCGAGGAGTAATGTCATCCACGTGTATATGCCGAACAAGAGCTTC
droFic1	scf7180000454039:613684-613831 -		AGCCAGC---------------**--------**AGTCAAC------GCCGCCCACTAAAAATGAGATGTGAGTTTT------GGG-TTTCT----CC-A--G--T----------**-ATT**---CTAGCTC--A-----GA---AAA--CTTAAT-A---AAA-----TGT-CTT--CTTT-----TTCAGTATTGCCGGAGGAATACCTCATCCACGTGCATATGCCGAACAAGAGCTTT
droEle1	scf7180000491201:1770649-1770804 -		AGCCAGC---------------**--------**AGTCAAC------GCCGCCCACTAAAAATGAGATGTGAGTTTT------GGG-TTTGG----CC-TCGATT-----------**GG--**GCCATCGCATC--AC----TA---AAA--CTGCAT-G---TCT-----GTT-TTTT--TTTC-----TACAGTAGTCCCGGAGGAGTACCTCATCCACGTGCATATGCCGAACAAAAGCTTT
droRho1	scf7180000780066:321261-321413 +		AGCCAGC---------------**--------**AGTCAAC------GCCGCCCACTAAAAATGAGATGTGAGTTTT------GGG-TTTGG----CT-TCGCTG-----------**GG--**ATCATCTTACC--A-----CA---AAATATACAAC-A---AC-----**---**ATG--CTTT-----TTCAGTACTCCCGGAGGAGTACCTCATCCACGTGCATATGCCGAACAAGAGCTTC
droBia1	scf7180000302143:2798240-2798388 -		AGCCAGC---------------**--------**AGTCAAC------GCCGCCCACTAAAAATGAGATGTGAGTTTC------CAG-TGTCG----------CTCC----------**--**----GATTGTTTC--G-----TG---TAA--CTGA-T-G---AAATGACAC---T-TCTTATC----CTTAGTATTCCCGGAGGAGTACCTCATCCACGTGCATATGCCGAACAAGAGCTTC
droTak1	scf7180000415379:181556-181704 -		AGCCAGC---------------**--------**AGTCAAC------GCCGCCCACTAAAAATGAGATGTGAGTTTC------GAG-ATGG----CC-CTCCTCC----------**--**----GATTGGTTT-A-----CT---AAG--ATAAA--**--**---CTCGA-T---TTC---TTTC-----TGCAGTATTCCCGGAGGAGTACCTCATCCACGTGCATATGCCGAACAAGAGCTTT
droEug1	scf7180000409474:2632373-2632522 +		AGCCAGC---------------**--------**AGTCAAC------ACCGCCCACTAAAAATGAGATGTGAGTTTT------GGT-CTCTT----------ACTTC----------**--**----GATT----TCGGACC--A-----CA---AAA--CTAAAT-G---AAA-----TAT-ATG--CTTC-----AACAGTATTGCTCGAGGAGTATCTCATCCACGTGCATATGCCGAACAAGAGCTTC
dm3	chr2R:15323935-15324087 -		AGCCACC---------------**--------**AGTCAAC------GCCGCCCAGTAAAAATGAGAGTGAGTTAT------GCCATTGG----CC-CCATAC----------**--**----CACCACATC--A-----TA---AAA--CTAAAT-G---AAA-----TCT-ATT--CCCC-----GCCAGTTAACTCCGAGGAGTATCTCATCCACGTGCATATGCCGAACAAGAGCTTC
droSim2	2r:15975683-15975833 -		AGCCACC---------------**--------**AGTCAAC------GCCGCCCAGTAAAAATGAGAGTGAGTTAT------GCT-CTTGG----CC-C-CCTAC----------**--**----CACCACACC--A-----TA---AAA--CTAAAT-G---AAA-----TCT-ATT--CCCC-----GCCAGTTCACTCCGAGGAGTATCTCATCCACGTGCATATGCCGAACAAGAGCTTC
droSec2	scaffold_1:12839940-12840091 -		AGCCACC---------------**--------**AGTCAAC------GCCGCCCAGTAAAAATGAGAGTGAGTTAT------GCT-CTTGG----CC-CCCCTAC----------**--**----CACCACACC--A-----TA---AAA--CTAAAT-G---AAA-----TCT-ATT--CCCC-----GCCAGTTCACTCCGAGGAGTATCTCATCCACGTGCATATGCCGAACAAGAGCTTC
droYak3	2R:13852461-13852609 +		AGCCACC---------------**--------**AGTCAAC------GCCGCCCACCAAAAATGAGAGTGAGTTAT------ACA-CTTGG----CC-A--G---**--**----------**--**AG--CCCC---**--**TC--A-----TA---ACA--CTAAATTG---A-ATCG--**-TATTT--TGTC-----GCCAGCACACTCCGAGGAGTATCTCATCCATGTGCATATGCCGAACAAGAGCTTT
droEre2	scaffold_4845:9522588-9522735 -		AGCCACC---------------**--------**AGTCAAC------GCCGCCCACCAAAAATGAGAGTGAGTTAT------GCA-CTTGG----CC-A--G---**--**----------**--**-------TGCCCCACA-----TA---AAA--CTAAAT-A---GTATCG--**-TATTT--GCTC-----GCCAGCACACTCCGAGGAGTATCTCATCCACGTGCATATGCCGAACAAGAGCTTT

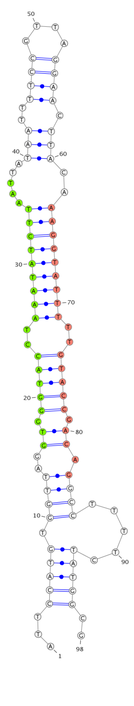
Generated: 09/08/2015 at 07:06 PM

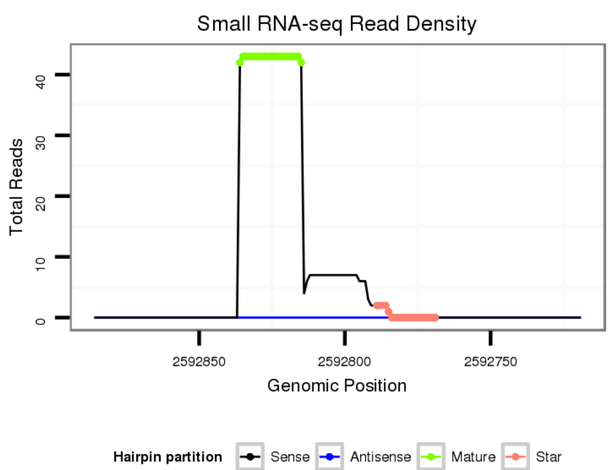
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

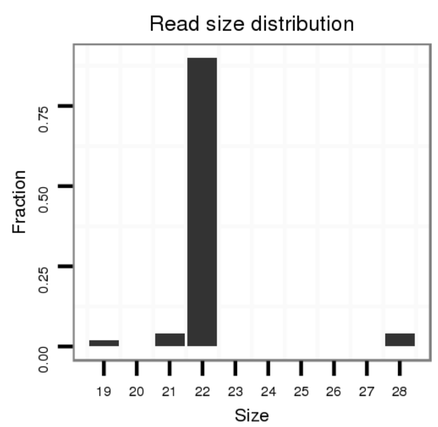
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_239	**4_group1:2592769-2592836 -**	**candidate**	**Mirtron**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

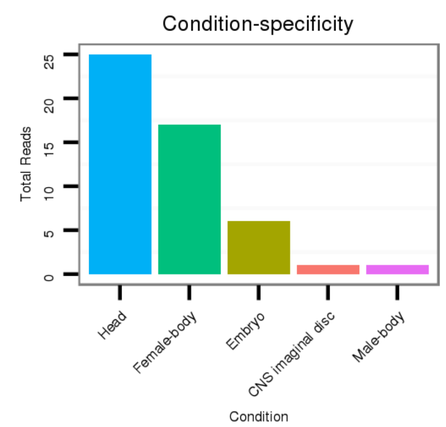
Legend: mature star mismatch in alignment mismatch in read

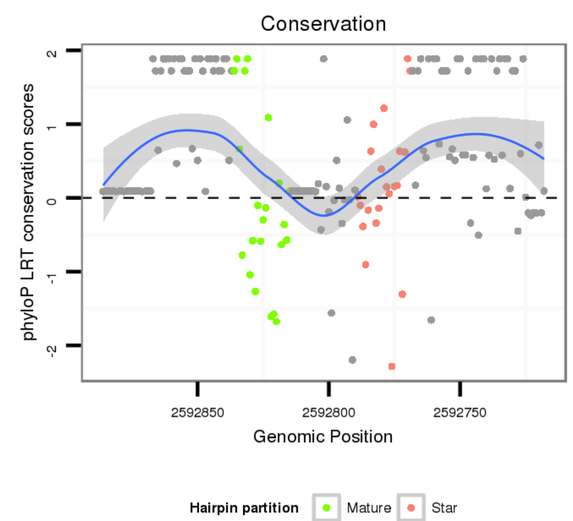
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCTATTCCATGTGGTTAGGTGGGTACCTAAATATCTTAATTATAATTTTCCGTTAGGAACTTACAAAGGTATTTTTGTACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATTCTGGTGTTTGGCCTACATCTA ********...(((((.((((..((.(((((..(((((((((.....(((..((((....)))).))).))..)))))))))..)))))..)).)).)))).....)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M062 head	M040 female body	M059 embryo	GSM444067 head	GSM343916 embryo	SRR902012 CNS imaginal disc	V112 male body
.....GTGGGTACCTAAATATCTTAAT.....	22	0	1	41.00	41	15	13	5	5	1	1	1
.....TATAATTTTCCGTTAGGAACTT.....	22	0	1	3.00	3	1	1	0	1	0	0	0
.....AAGGTATTTTTGTACCGACAGC.....	22	1	1	1.00	1	0	0	1	0	0	0	0
.....GTGGGTACCTAAATATCTTAAC.....	22	1	1	1.00	1	0	0	1	0	0	0	0
.....GTGGGTACCTAAATATCTTAA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TGGGTACCTAAATATCTTAAT.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....TAATTTTCCGTTAGGAACTTACAAAGGT.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....TATAATTTTCCGTTAGGAA.....	19	0	1	1.00	1	0	1	0	0	0	0	0
.....ATAATTTTCCGTTAGGAACTTACAAAGG.....	28	0	1	1.00	1	0	1	0	0	0	0	0
.....ATAATTTTCCGTTAGGAACTTA.....	22	0	1	1.00	1	0	0	0	1	0	0	0

Anti-sense strand reads

GAAAACATCTAAAAAGTATACACTTTCAGTTGCGATAAGGTACACCAATCCACCCATGGATTTATAGAATTAATATTAAAAGGCAATCCTTGAATGTTTCCATAAAAACATGGCTGTCCGGAAAAGATACCGCGATTTTCGTATTAAGACCACAAACCGGATGTAGAT ********...(((((.((((..((.(((((..(((((((((.....(((..((((....)))).))).))..)))))))))..)))))..)).)).)))).....)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group1:2592718-2592886 -	dps_239	CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCTATTCCATGTGGTTAGGTGGGTACCTAAA-TATCTTAATTATAATTTTCCGTT---AGGAACTTA----------CA----------A-AG--GTA--TTTTTGT-----ACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATTCTGGTGTTTGGCCTACATCTAT
droPer2	scaffold_5:2613064-2613232 +	dpe_2487	CTTTTGTAGATTTTTCATATGTGAAAGTCAACGCAATTCCATGTGGTTAGGTGGGTACCTAAA-TATCTTAATTATAATTTTCCGTT---AGGAACTTA----------CA----------A-AG--GTA--TTTTTGT-----ACCGACAGGCCTTTTCTATGGCGCTAAAAGCATAATTCTGGTGTTTGGCATACATCTAT
droVir3	scaffold_12963:4588916-4589061 -		----------TGCGAAAGTGAACGCAATTCCATGTGGTTAGGTATGTTG-CCAG-CTATACA----------TT---TATATCTTTTGATATT-----ACATTGAT---TATT-----T-TT--TATTTTTTTAT-----TTTTGCAGGACTTGTCTATGGCGTTAAGGGTCTGATACTTGTATTCGGTCT--------
droMoj3	scaffold_6500:8495806-8495947 -		----------TGCGAAAGTGAACGCAATTCTATGTGGTTAGGTAAGTACTTCAA-TATCTATT----------TC---A---AAT--------TCGTTTT-AATTAAT----------C-GTCCACTT-ACT---------TTTTGCAGGACTTGTTTATGGCGTTAAGGGTCTTATATTGGTATTTGGTCTGTTCTTG-
droKik1	scf7180000302235:132561-132702 -		----------TGTGAAAGTCAACGCAACTCAATGTGGTTGGGTACGTACCTATTT-CATTT----------TGTTATTAAGAAAT----------TCCT-TTAT----AT-AA-AG--TTA--TC--TGGACTTTTTTTCAGGTCTTGTTTATGGCTTCAAGGGCCTGATCCTGGTGTTTGGTCT--------
droFic1	scf7180000453316:79293-79433 +		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTATGTTTTTAATC-AGTTT----------GTTT---AGGAAAT----------TTA-TGTTA----CTATTAATTAA-T---GAATT-ATC---------CCTTCTAGGTCTTGTCTATGGCTTCAAGGGACTAATCCTGGTGTTTGGTCTA--------
droEle1	scf7180000491046:1482269-1482406 +		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTATGTACCAAAAG-CGCTC----------GTTT---TCGAACA----------AAACTCT-TACT----AT-AA-TG--GAAT-------ATCTAATATTCAGGTCTTGTGTATGGCTTCAAGGGCCTAATCCTGGTGTTTGGCCT--------
droBia1	scf7180000302261:1570768-1570902 -		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTAGGTCTTACATA-TAAAT----------GTTT---AAGAG----------CC-----GAACTAAT----------A-GTAATATT-ACTTGT-----GTTTTCAGGTCTCGTCTACGGCTTCAAGGGCCTGATCCTGGTGTTCGGCCT--------
droTak1	scf7180000412373:124394-124534 +		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTATGTCATATAAT-CTATACT----------TG---T---AGG----------ATTTTTT-GATTAA----TATT-AT-AA-TT--TAAT-------ATTTATTTACAGGTCTCGTTTATGGCTTCAAGGGCCTAATCCTGGTGTTTGGCCT--------
droSec2	scaffold_3:1292333-1292466 +		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTATGTTGTGATAT-CGGTA----------GATT---AGGAAGATA----------CA--------TATA-AT-ATA-TTAATATT-A-----CTTTGCAGGTCTTGTATATGGCTTCAAGGGCCTAATCCTGGTGTTTGGCCT--------
droYak3	2L:15139031-15139160 +		----------TGTGAAAGTCAACGCAACTCCATGTGGTTGGGTATGTGCAAAA-TATGCACA----------TT---AATCAGA----------TATAAT----------A-TTTATATT-ATT---------TTTTTCAGGTCTTGTATATGGCTTCAAGGGCCTAATCCTGGTGTTTGGTCT--------

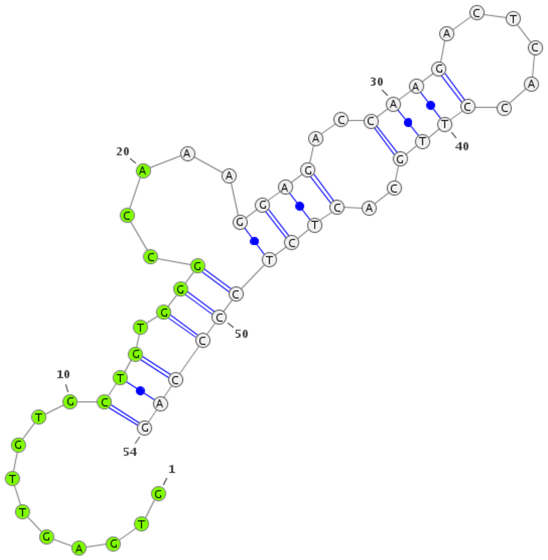
Generated: 09/08/2015 at 08:16 PM

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

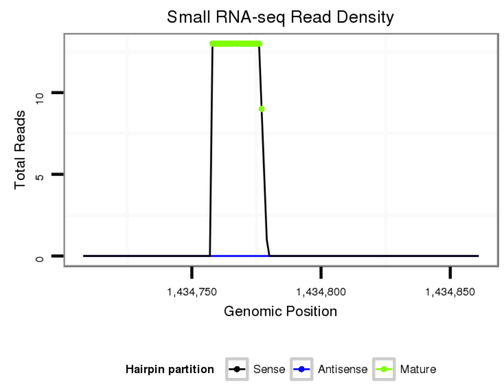
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_934	**3:1434758-1434811 +**	**candidate**	**Mirtron**	**3pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

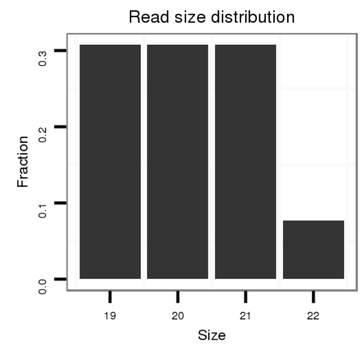
Legend: mature star mismatch in alignment mismatch in read

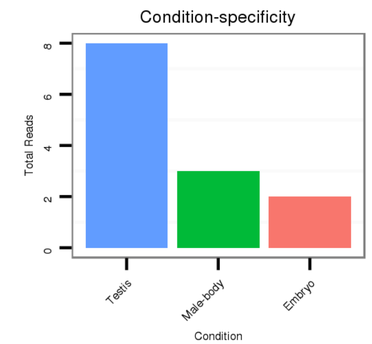
Predicted structure

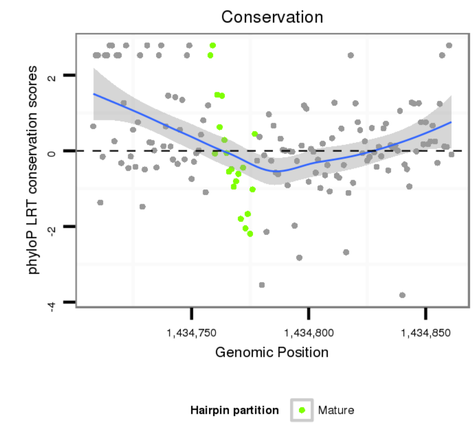


dps_934_annot [-12.4]









Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_1797]; intron [Dpse\GA24631-in]; CDS [Dpse\GA24631-cds]; CDS [Dpse\GA24631-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       
GCGTCCCAAACGGCTGACCGCTCTGACTGAGAAACACAGATGATTCCCAAGGTGAGTTGTGCTGTGGGCCAAAGGAGACCAAGACTCACCTTGCACTCTCCCCAGATGCCCCCGACGTCACGGCAGAGTCCTCGGGCCGCCAAAGTGCGCGGTTG
**********************************************************..........(((.(((.....((((..((((......))))..)))))))))))**********************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	SRR902011 testis	M022 male body	M059 embryo	GSM444067 head	
20	0	1	4.00	4	0	0	3	0	1	0	....GTGAGTTGTGCTGTGGGCCA....
21	0	1	4.00	4	0	1	3	0	0	0	....GTGAGTTGTGCTGTGGGCCAA....
19	0	1	4.00	4	0	1	2	0	1	0	....GTGAGTTGTGCTGTGGGCC....
22	0	1	1.00	1	0	1	0	0	0	0	....GTGAGTTGTGCTGTGGGCCAAA....
28	1	2	0.50	1	0	0	0	0	1	0	GCGTCCCAAACGGCTGACCGCTCTGACG....
27	0	2	0.50	1	0	0	1	0	0	0	.....TGACCGCTCTGACTGAGAACACAGATG....

Anti-sense strand reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
CGCAGGGTTTGCCGACTGGCGAGACTGACTCTTGTGTCTACTAAGGGTTCCACTCAACACGACACCCGGTTTCCTCTGGTTCTGAGTGGAACGTGAGAGGGGTCTACGGGGGCTGCAGTGCCGTCTCAGGAGCCCGGCGGTTTCACGCGCCAAC
**************************************************.........(((.(((.....((((..((((......))))..)))))))))))**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM343916 embryo	M022 male body	GSM444067 head	SRR902010 ovaries	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:1434708-1434861 +	dps_934	GCGTCCCAAACGGCTGACCGCTCTGACTGAGAAACACAGATGATTCCCAAGGTGAGTT-----GTGCTG-TGGGC-C-----AAAGGA----------GACCAA---GA-CTCACC----------TTG-----CACTCTCCCCAGATGCCCCCGACGTCACGGCA----------GAG---TCCTCGGGCCGCCAAAGTGCGCGGTTG
droPer2	scaffold_2:1608114-1608267 +	dpe_2485	GCGTCCCAAACGGCTGACCGCTCTGACTGAGAAACACAGATGATTCCCAAGGTGAGTT-----GTGCTG-TGGGC-C-----AAAGGA----------GACCAA---GA-CTCACC----------TTG-----CACTCTCCCCAGATGCCCCCGACGTCACGGCA----------GAG---TCCTCGGGCCGCCAAAGTGCGCGGTTG
droWil2	scf2_1100000004513:2801067-2801223 +		GCGTCCCAAGCGCTGACTTGATATGGAAAACGAGCATGAAAGT---GTTGAGTA-----AAGCAA-TTTT-T-------AACAAATTCCACT-------AAAA------A-GTGATAATA------AATT-----AATGATTTATCAGAGATGATGCTCGATG----------GAA---TACAGTGTGCGCCAGTGCGCGCAATG
droVir3	scaffold_12875:1586889-1587036 -		GCGACCCAAGCGCTGACGTGCCTTGTCGAAGATGATGCGA------CGGTAAGTT-----GTGAAA-TGATT-A-----AGTCGA----------GTGCA---AA-CTCATT----------TTG-----GCGCCTTGCAGAAGAGTGCAATTGCGCGCAGC----------GAG---GTCTCACAGCGCCAGAGGCAGCGATG
droMoj3	scaffold_6496:4698604-4698759 -		GCGAGCCAAGCGCTTGACGTCTTTAGCTGAGGATGATGCGA------TGGTAAATTGTGAAA-TAAA-ATCCA-AGT--GAAATGT---TCCATGC-----T-----------AA-----T---TT----------ATAT-----------AC-TAAATAGCACCCGCAGATGTCCGCGAT----------ATCCAGGTCGACAGCGACAGAGCGCTCGCTTG
droGri2	scaffold_15245:9414646-9414813 +		AGGTGCCAAGCGCTCGATGATGTTGAAGTCGAAGCGA------TGGTGAGCT-----GTGAAA-AA-TT-CAA-A---AGAACTAAAATA-------ACTC------A-CTCAAATTACTGATCCATT--TTGCG---CAGTTCCGTGTGATGCATCGTGCCTCTAGC----------GAG---TCTTCCGAGCGCCAGAGCGCTCGCATA
droAna3	scaffold_13266:3379784-3379934 +		GCGCCCCAAACCATTAGCTCTCTGATTGAGGATAAGGATGAGCCTCAAGGTAAGTC-----TCCTGC-CCTGC-TGT-A---TGCG------C------------C------T-TCTCTACA------TCCT-----------TCTTTGCCAATATGGCCGACACAACAACG----------AAT---TCCACGTACGCCAGATCGCAAGGATC
droBip1	scf7180000396427:1846735-1846889 +		GCGCCCCAAACGGCTTAGTTCCTGATCGAGGACCAGGAGAGGCCTCAAGGTAAGTC-----TTCTGG-TGGCT-C-----GAATGT--ATGCGGCT----------GA---T---TTACTA------TCCG-----------TCTTTACCAACATAAGAGACACCACAACG----------AAT---TCCACGGTACGCCAGAGCGCAAGGATT
droKik1	scf7180000302640:268567-268711 +		GCGCCCCAAGCGCTCTCCTCTTCTGGTCGAGGACAAGGAGAGCTCCAGGGTGAGTA-----TCATCC-CC---T---GAGTCCGAACCGACGCTGAGACCAGTACTGACTTCCGACAATCGTCAGCCAAC---TCGTCAACTCGACAGAGCATCGGCTC
droFic1	scf7180000453955:106246-106407 -		GCGACCCAAACGCTCACCTCCTGGCCGAGGATCATGACGAACACCAGGGTGAGTA-----TGCAGC-TGAT-T-----GAAATCT---ACCGAGC------TG----G-----------G---GTA----------AGACCTGGATTCTATCCTTTTCAGTTGGTCCCGACACAACGGCG----------AAC---TCCTCCAGGTTCCAAACCCGTTCGGCTC
droEle1	scf7180000491265:302934-303083 +		GCGCCCCAAGCGCTGAGCTCTTTGCCGAGGATGAGGACGACTCCCAAGGTGAGTA-----TCTCTG-CCCAC-TGG-G---GAATCTTCCGTGC-------GAGT------G-CCCGAT-A------ACGA-----------TCCTTATTTCAGTCCCGACACCACG--SCTCGCCGAGCGTGCGCGTA
droRho1	scf7180000779390:20784-20936 +		GCGCCCCAAGCGCTGAGCTCTTCGCTGAGGATCAGGACGACTCCGAGGGTGAGTA-----TCCTCG-TCCACA-TGA-A---CGC-------CC-----------------C---AGCCCATCT-A------ATGA-----------TCTATTTAGCTGCCACCGACACCACGGCG----------AGC---TCTCGGCCGGCCGCCAGATTCGGCTC
droBia1	scf7180000302292:2983537-2983702 -		GCGCCCCAAGCGCTCTCCTCCTGGCCGAAGATCACGACGACCCCATATGTGAGTA-----TACTCG-TCTCGCCGACCGACAGGC------ACCT-----------------GGCTAA-CACATTGCCA------ATGT-----------TTCCTTTCAGCTGTCCCCGACACCACGGTC----------AATACCACCACCACTCGCACGAGCGCTCGGCTC
droTak1	scf7180000411052:20260-20423 -		GCGCCCCAAGCGCTCACCTCCTGGCCGAGGATCAGGATGAGGCGGGAAAGTGAGTA-----TTCCAG-GCAGC-A-GCG---ACGAGGAGCACCT-------TCCT------A-ATCCACCG------CCCT-----------TCCCTTCCAGCTGGTCCCGACACCACGACG----------AACACCTCCTCACTCCGCCAGAGCGCTGGGCTC
droEug1	scf7180000409672:5175967-5176134 +		ACCCCCCAAGCGCTCTAATATTGCCGAGGATCAGGAGCACACGGGCGTATTA-----TTGGAC-ACTA-TATCC---CGATAGATCAATATCATACA-AACA------T-TATCCATC-T------ATCT-----------TTACTTTTAGCAGCCCCCGACGTTAAGGCG----------AAC---TCCTCTCTCCGCAAGCCGTTCGTGCTC
dm3	chr2R:3166497-3166661 +		GCGCCCCAAGCGCTCACCTCATCGCCGAGGATCAGAATGAGCCCCACGGGTGAGTA-----TCCTGC-CCATT-TTA-A---ACCATTAACGACC-------AACA------A-CCCTGT-G------ATAT-----------TCCATTTGAGCAGCTCCAGACGCCACGGCG----------AACAACACGTCGGCCCGTCAAAGCATCGGCTC
droSim2	2r:3991942-3992106 +		GCGCCCCAAGCGCTCACCTCATCGCCGAGGATCAGAATGAGCCCCACGGGTGAGTA-----TCCTGC-CCATT-TTA-A---ACCGTTAACGACC-------AACT------A-CCCTGT-G------ATAT-----------TCCATTTGAGCAGCTCCAGACGCCACGGCG----------AACAACACGTCGGCCCGTCAAAGCATCGGCTC
droYak3	scaffold_11310865:1089829 + 2L:15853445-15853594 +		GCGCCCCAAGCGCTCTCCTCATCGCCGAGGATCAGAATGAGCCCCACGGGTACGTA-----ACCTCG-CCATC-TTA-A---TGTTTAAAAGGCG-------AAAT------A-TCCCTTTTG------ATAT-----------TCCATTTATCAGCGTCCAGACGCCACGGCG----------AAC---TCCTCACGCCGTCAAAGCATCGGCTC
droEre2	scaffold_4929:19427227-19427388 -		GCGCCCCAAGCGCTCACCTCATCGCCGAGGATCAGAATGAGCCCCACGGGTGAGTA-----ACCTCG-CCATC-TTA-T---TGCTTAAAAGGAA-------AACT------A-TCCCTTTG------ATAT-----------TCCATTTAGCAAGTCCAGACGCCACGGCG----------AAC---TCCTCACGCCGTCAAAGCATCGGCTC

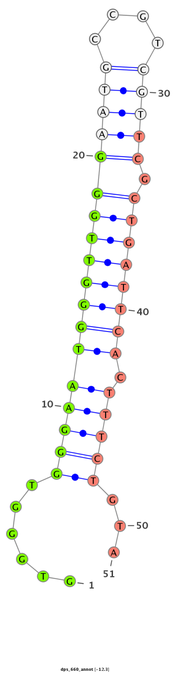
Generated: 09/08/2015 at 07:03 PM

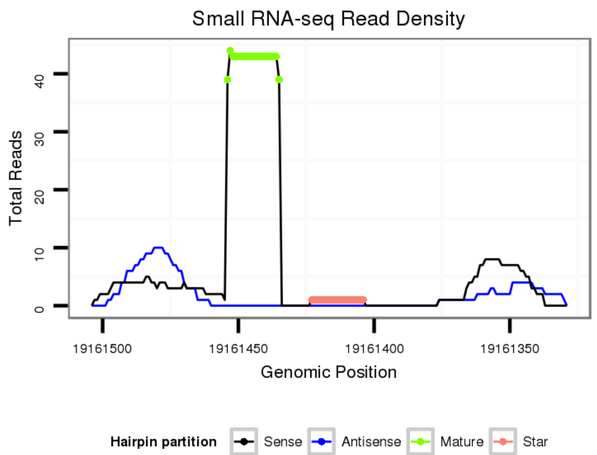
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

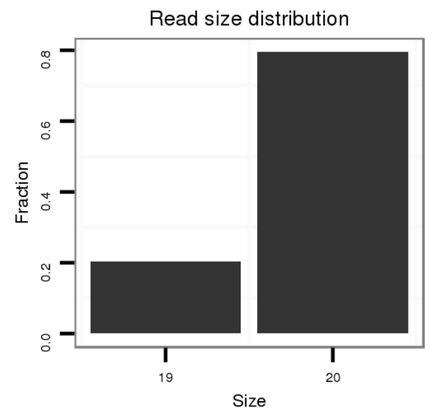
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_660	**2:19161379-19161454 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

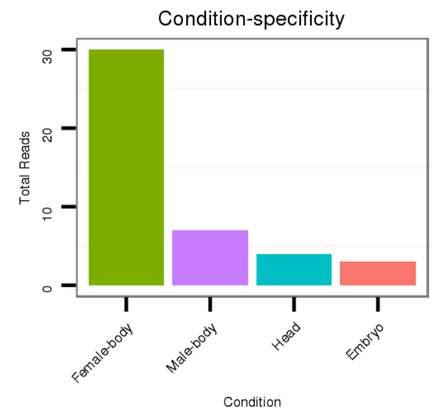
Legend: mature star mismatch in alignment mismatch in read

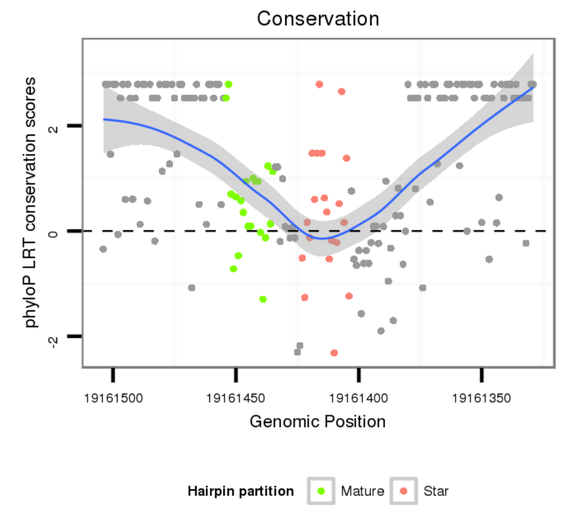
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GA13067-in]; CDS [Dpse\GA13067-cds]; CDS [Dpse\GA13067-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAAAATTCAGACGCTCAAGTCCCAGAACACAATGGCCCAGGCAATGAAAGGTGGGTGGGAATGGGTTGGGAATGCCGTCGTTCGCTGATTCACTTTCTGTAATCTTGGAATTTTCCCTATTTTTAGGTGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCACAA **********.....(((((((((((((((((....)))))).)))))))).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M059 embryo	SRR902011 testis	GSM444067 head	GSM343916 embryo	M062 head
.....GTGGGTGGGAATGGGTTGGG.....	20	0	1	34.00	34	23	7	1	0	1	1	1
.....TGGGTGGGAATGGGTTGGG.....	19	0	1	5.00	5	2	0	1	0	2	0	0
.....GTGGGTGGGAATGGGTTGG.....	19	0	1	4.00	4	4	0	0	0	0	0	0
.....CAGAACATGAACCGCCAGC.....	19	0	1	2.00	2	0	0	0	2	0	0	0
.....GTCACCAAGGCCATGCAGAACAT.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....TCGCTGATTCACTTTCTGTA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....AGACGCTCAAGTCCCAGAAC.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....CCATGCAGAACATGAACCGCCAGCTG.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....CCATGCAGAACATGAACCGC.....	20	0	1	1.00	1	0	0	0	1	0	0	0
.....GAACATGAACCGCCAGCTGAAT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AACACAATGGCCCAGGCAATGAAA.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....CCCAGAACACAATGGCCCAGGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0
...AATTCAGACGCTCAAGTCCCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.AAAATTCAGACGCTCAAGTCC.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....GCCCAGGCAATGAAAGGT.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....TGCAGAACATGAACCGCCA.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....CATGCAGAACATGAACCGCCAGCTGAAT.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....CAGACGCTCAAGTCCCAGAACACAATGG.....	28	0	1	1.00	1	1	0	0	0	0	0	0
.....GGTGGGAATGGGTTGGGGT.....	19	2	20	0.05	1	0	1	0	0	0	0	0

Anti-sense strand reads

GTTTTAAGTCTGCGAGTTCAGGGTCTTGTGTTACCGGGTCCGTTACTTTCCACCCACCCTTACCCAACCCTTACGGCAGCAAGCGACTAAGTGAAAGACATTAGAACCTTAAAAGGGATAAAAATCCACAGTGGTTCCGGTACGTCTTGTACTTGGCGGTCGACTTAGAGGGTGTT **********.....(((((((((((((((((....)))))).)))))))).)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V112 male body	M040 female body	SRR902011 testis	M022 male body	M059 embryo	GSM343916 embryo
.....GAGTTCAGGGTCTTGTGTTAC.....	21	0	1	2.00	2	0	0	2	0	0	0
.....GCGGTCGACTTAGAGGGTGT.	20	0	1	1.00	1	0	1	0	0	0	0
.....GGGTCTTGTGTTACCGGGT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TCTGCGAGTTCAGGGTCTTGT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTCAGGGTCTTGTGTTACC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TCTTGTGTTACCGGGTCCGTT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CAGGGTCTTGTGTTACCGGGT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CAGTGGTTCCGGTACGTCTTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGTACTTGGCGGTCGACTTA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTGAGTTCAGGGTCTTGTGTT.....	21	2	1	1.00	1	1	0	0	0	0	0
.....GCGAGTTCAGGGTCTTGTGTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CGTCTTGTACTTGGCGGTCGA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GCGAGTTCAGGGTCTTGTG.....	19	0	1	1.00	1	0	0	1	0	0	0
.....AGTCTGCGAGTTCAGGGTCTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GCGGTCGACTTAGAGGGTG..	19	0	1	1.00	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:19161329-19161504 -	dps_660	CAAAATTCAGACGCTCAAGTCCCAGAACACAATGGCCCAGGCAATGAAAGGTGGGTG----------GGAATGGGTTGGG-AATGCCGT--------C-GTTCGCTGATTCACT---TTCT-GTAATCTTGGAATTTTCCCT--ATTTTTAGGTGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCACAA
droPer2	scaffold_3:1906604-1906779 -	dpe_1364	CAAAATTCAGACGCTCAAGTCCCAGAACACAATGGCCCAGGCAATGAAAGGTGGGTG----------GGAATGGGATGGG-AATGCCGT--------C-GTTCGCTGATTCACT---TTCT-GTAATCTTGGAATTTTCCCT--ATTTTTAGGTGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCACAA
droWil2	scf2_1100000004943:15508471-15508646 +		GAAAATCCAGACGCTAAATCCCAAACACAATGGCACAGGCAATGAAAGGTGCGTCAATCGAATGATTGGGG--TGGACTGGGTAAT---AC--------CTGTCAGCTGATTCATG---CTATTATCTA----------T-TCCTTACAGGTGTGACCAAGGCCATGCAGAATATGAATCGTCAATTGAATCTCCCGCAA
droVir3	scaffold_13047:5463216-5463375 +		AAAAATACAAACGCTTAAATCTCAAAACACAATGGCCCAAGCAATGAAAGGTGTGGG----------AGG---G-T---TTG--CCCATGCGTGATTCATATTTTACT---CATCC-G-----TC-CCTATATTTGTAGGTGTCACCAAGGCCATGCAGAATATGAATCGCAGAACTGAATCTCCCGCAA
droMoj3	scaffold_6540:15835996-15836159 +		TAAAATACAAACGCTTAAATCTCAAAACACAATGGCCCAAGCAATGAAAGGTGAGG----------G-------A-GAG-AAGG-TTT--------CCAATGATGATTCAGAATTTACTTATGATATCG---------TTATTTTCGCAGGTGTCACCAAGGCCATGCAGAACATGAATCGTCAATTGAATCTCCCGCAA
droGri2	scaffold_14906:10837383-10837547 +		TAAGATACAAACGCTCAAATCTCAAAACACAATGGCACAGGCCATGAAAGGTGGGTG----------GG--TGGCAGGGG-AA-G-CAC--------C-ATTTCGTGATTCACA-----------TTTGGCTAATG--CG-TTT-CGTTTGCAGGTGTGACAAAGGCCATGCAGAACATGAACCGCGAACTGAATCTCCCGCAA
droAna3	scaffold_13340:11264935-11265093 -		CAAAATACAAACTCTCAAATCCCAGAACACAATGGCCAGGCCATGAAGGGTAGGCG----------C----------------AT--------CTGACAGCTGATTCAGT---AGCTTATTATCTCAACT--TT-CAAACCTTCGCAGGTGTCACCAAAGCCATGCAGAATATGAACCGCGAACTGAATCTCCCGCAA
droBip1	scf7180000396691:174774-174932 -		CAAAATACAAACTCTCAAATCCCAGAACACAATGGCCAGGCCATGAAGGGTAGGCG----------------------CAT--------CTATCAGCTGATTCAGT---AGCTTATCATCTTAATT--TT-CAAACCTTGCAGGTGTCACCAAGCCATGCAGAATATGAATCGCCAGCTGAATCTCCCACAA
droKik1	scf7180000302261:72210-72363 -		CAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCACAGGCTATGAAGGGTGGGTG----------G----------------------------AT-CACCTGATTATT---AACTTTTCATACTGAAT--CC-CCT-TTTTTTTAGGCGTGACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droFic1	scf7180000454055:1788061-1788213 +		CAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCCCAAGCCATGAAGGGTAAACA----------------------------------GGTGCCTTTTTTTT---TGCTTATCAGCTACTAA--AA-CGC-CCTTTTTAGGTGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCACAA
droEle1	scf7180000491261:828615-828774 -		CAAAATCCAGACGCTCAAGTCTCAGAACACAATGGCACAGGCCATGAAGGGTAA-CA----------------------------TACATAG--C-GTCAGCTGATTCATT---AGCTTATCATCCCGTAA--AC-CCC-ATTTCCCAGGTGTTACCAAGGCCATGCAAAACATGAACCGCCAGCTGAATCTCCCACAA
droRho1	scf7180000780074:230255-230413 +		TAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCACAGGCCATGAAGGGTAAGTA----------------------------------CACA-CATGCGACTGATTCATT---TGCTTATCATTTCGTAA--AA-CCT-TTTTCCCAGGTGTTACCAAGGCCATGCAAAACATGAACCGTCAGCTGAATCTCCCGCAA
droBia1	scf7180000302113:2080981-2081140 +		CAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCGCAGGCCATGAAGGGTAGATA----------------------------TGGGTTAATCAGCTCATCCTTA---GCCTTACTAACTTCATG--TA-CTC-CCCATCCAGGTGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droTak1	scf7180000415851:298182-298332 -		CAAAATCCAGACGCTCAAGTCGCAGAATACCATGGCCAGGCCATGAAGGGTAAATA----------------------------CTGGGCCTATAGATGATTCACT---CATTCATAAC----------CTT-ATCTTTCAGGCGTCACCAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droEug1	scf7180000409682:733718-733876 -		TAAAATCCAGACTCTCAAGTCGCAGAACACAATGGCACAGGCCATGAAAGGTAAATA----------------------------TTGCACATTTAGGTGATTCATT---AGCTTCTTATCTTAAAA--TT-CC--TCTTTTCAGGTGTAACGAAGGCCATGCAGAATATGAACCGCCAGCTGAATCTCCCACAA
dm3	chr3R:21878902-21879061 +		CAAAATTCAGACGCTCAAGTCGCAGAACACAATGGCACAGGCCATGAAAGGTAAACA----------------------------TTGGCTATTTGGCTGATTCACC---CCCTTATCAAGCAATTA--TG-CTT-ATCTTCCAGGTGTCACGAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droSim2	3r:21376042-21376201 +		CAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCACAGGCCATGAAAGGTAAACA----------------------------TTGGCAGTGTAGCTGATTCACC---CCCTTATCAAGCAATTA--TG-CTT-ACCTTTCAGGTGTCACGAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droSec2	scaffold_13:673564-673723 +		CAAAATCCAGACGCTCAAGTCGCAGAACACAATGGCACAGGCCATGAAAGGTAGACA----------------------------TTGGCAGTGTAGCTGATTCACC---CCCTTATCAAGCAATTA--TG-CTT-ACCTTTCAGGTGTCACGAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droYak3	3R:24595725-24595884 -		CAAAATCCAGACGCTCAAGTCCCAGAACACAATGGCGCAGGCCATGAAAGGTAAACA----------------------------TTGGATACGCAGCTGATTCATC---GCCTTATCAACTGATTA--TG-CTC-GCTATTCAGGTGTTACGAAGGCCATGCAGAACATGAACCGCCAGCTGAATCTCCCGCAA
droEre2	scaffold_4820:6166087-6166246 -		CAAAATCCAGACGCTCAAGTCCCAGAACACAATGGCACAGGCCATGAAAGGTAAACA----------------------------TGGGACATGCGCTGATTCATT---GCCTTATCAACTGATTA--TG-CTC-GCTTTTCAGGTGTTACGAAGGCCATGCAGAACATGAACCGCCAACTGAATCTCCCGCAA

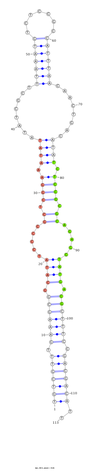
Generated: 09/08/2015 at 07:06 PM

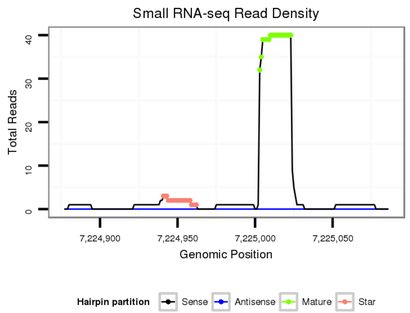
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

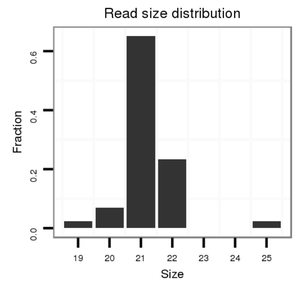
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3821	**XL_group1a:7224927-7225036 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

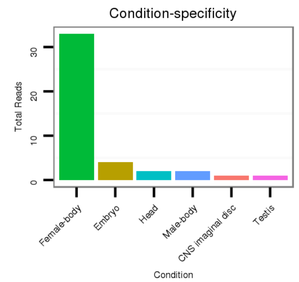
Legend: mature star mismatch in alignment mismatch in read

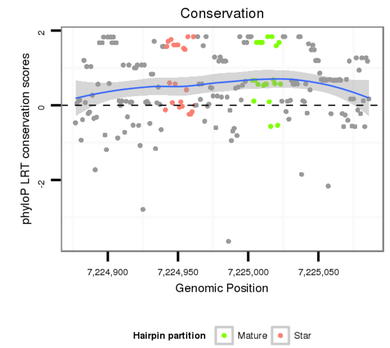
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCTCATGAACTGCCGGCGGAATTATGTCGCTTCTTTCTGGAGGACTTGTGTCGTTTGAAAGCGGCATATCCCCGCTCGGAAATATATCGCTTTAAATGTCTCCGCCATTTAACAACTGACATATCTCCGCGCAGAGCTATGACGCTTTCCGACGACATTTCGTCGGAGATATTGTCGATGCCCCCACAGTTCCATATAGCCATTTCA											SRR902012		
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	GSM444067 head	V112 male body	SRR902011 testis	CNS imaginal disc	GSM343916 embryo	M062 head
.....TCTCCGCGCAGAGCTATGACG.....	21	0	1	27.00	27	23	0	1	2	0	0	1	0
.....TCTCCGCGCAGAGCTATGACGC.....	22	0	1	4.00	4	3	1	0	0	0	0	0	0
.....ATGACGCTTTCCGACGACATG.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0
.....CTCCGCGCAGAGCTATGACG.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0
.....TCCGCGCAGAGCTATGACGCTT.....	22	0	1	2.00	2	2	0	0	0	0	0	0	0
...TCATGAACTGCCGGC.....	15	0	1	1.00	1	0	0	0	0	0	1	0	0
.....CTTGTGTCGTTTGAAAGCGGCA.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0
.....TCCGCGCAGAGCTATGACGCT.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TCCGCGCAGAGCTATGACG.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0
.....ATCTCCGCGCAGAGCTATGACG.....	22	0	1	1.00	1	0	0	0	0	0	0	1	0
.....TGTCGATGCCCCCACAGTTCCATATA.....	26	0	1	1.00	1	0	1	0	0	0	0	0	0
.....ATGTCTCCGCCATTTAACAACTGAC.....	25	0	1	1.00	1	0	0	0	0	0	1	0	0
.....GCATATCCCCGCTCGGAAATAT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....GCAGAGCTATGACGCTTTCCGA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0
.....TGACGCTTTCCGACGACATG.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0
.....CGGCATATCCCCGCTCGGAA.....	20	0	1	1.00	1	0	0	0	0	1	0	0	0
.....CTCCGCGCAGAGCTATGACGCT.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0
.....TGCCGGCGGAATTATGTCGCTT.....	22	0	8	0.13	1	1	0	0	0	0	0	0	0

Anti-sense strand reads

TCGAGTACTTGACGGCCGCCTTAATACAGCGAAGAAAGACCTCCTGAACACAGCAAACTTTCGCCGTATAGGGGCGAGCCTTTATATATAGCGAAATTTACAGAGGCGGTAAATTGTTGACTGTATAGAGGCGCGTCTCGATACTGCGAAAGGCTGCTGTAAAGCAGCCTCTATAACAGCTACGGGGGTGTCAAGGTATATCGGTAAAGT							
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902010 ovaries	M062 head
Show Alignment With Reads							

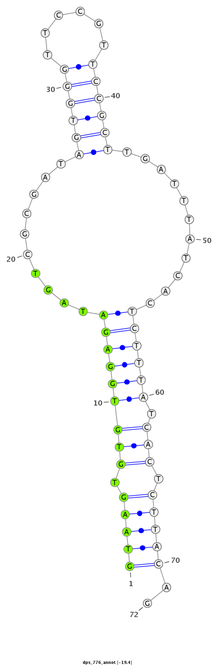
Re-alignment of all predicted orthologs

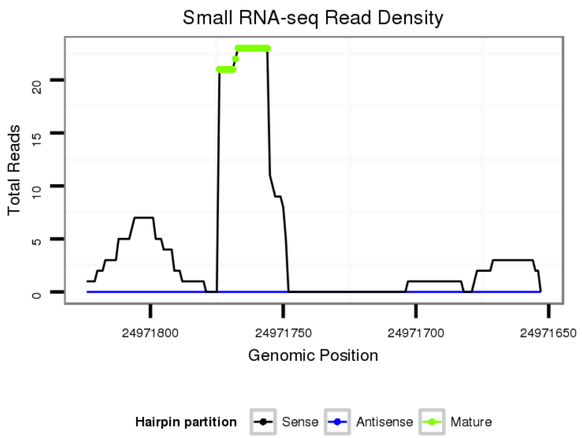
Species	Coordinate	ID	Alignment
dp5	XL_group1a:7224877-7225086 +	dps_3821	A-GCTC-----AT--GAACTGCCGGCGGAATTATGTCGCT-TCTTTCTGGAGGACTTGTGTCGTTTGAAAGC----------GGCA----------TATCCCCGCTCGG----------AAATATATATCGCTTT-AA-----AT---GTCTCCGCCATTTAACAACTGACATATCTCCGCGCAGAGCTATG---------ACGCTTTCCGACGACATTTCGTC---GGAG----------ATATTGTCGATGCCCC-CACAGTTCCATATAGCCATTTCA
droPer2	scaffold_13:1836381-1836572 +	dpe_143	A-GCTC-----AT--GAACTGC----------CT-CTTTCTGGAGGACTTGTGTCGTTTGAAAGC----------GTCA----------TATCCCCGCTCGG----------ACATAT--TATCGCTTT-AA-----AT---GTCTCCGCCGTTTAACAAAGGACATATCTCCGCGCAGAGCTAG---------ACGTTTCCGACGACATGTCGTC---GGAG----------ATATTGTCGTGCCCC-CACAGTTCCATATAGCCATTTCA
droWil2	scaf2_1100000004952:688234-688462 +		G-GCG-----GT--GATTG--GCGGGTATATGTCGT-----------GAAAC----------GTGAATCTCGCCGTTAAAAAACGACATATCGCGGGGA----------AATAA--TGCGTTT-AG-------GT---------AACGACATATCTCCGCGGAATATGTATG---------TCGTTTCAGAACGACATATGTCGCGGCGGAGATATGTCGTTTTTCTAACGGCGGAGATATGTCGC----------CGGAGATA-TGTCGTATCCCGCACGCATACATA--CATTCA
droVir3	scaffold_13042:2246335-2246566 +		G-----------G--------CGCGGGTTTGTGTCGT-----------CTCCACGTCATATCTCCCGTGGAGTTATGTCGTTTTGAAACGTGA----------TATCTGCCGCGGGAGTTATATCGTTTTAGAACATCATTATCTCGCGCGGGTGTCA--TGCGTT--T--------GT---------TTGAACACGCATATCTCCGCGCGAGTTATG---------TCGTTTTAGAACATCATTATCTGTCGCGCGGAG----------TTATGTCGTT--TTAGAACATCACATTTCCG-----GCGGAGCTATGTCG
droKik1	scaf7180000302704:11142-11349 +		G-----------G--------GCGGGTTTATGTCGCT-----------GAAAC----------GACGTATCTCCGCCAAACTAGAAACGACATATCTCGCGGGG----------GTGTA--TGCGCCTGT-AAGCGACAT----ATCTCCGCCGAACTAGAAAGGACATATCTCCGCGCGGAGCTATG---------TCGTTTAAAGTGACATAAGTCGCGGCGGAG----------GTATGTCGTTGCTTACGACA--ACAGCTCCC-----GCGAATTCTATCA
droRho1	scaf7180000760199:17228-17397 -		T-----------G--------GCGGGGGATTATGTCGTCATTTTATTGGCGGGATTTGTATTTTAAATGC----------GACA----------GAGTGCGC-----ATTGACTACGCGGAAGGG--TGCGCTTGTAAAACGACAT----ATCTCCGCCGTTCTACAAAGGACATATCTCCGCGGGGAGATA---------TCGTTTTAAAACGACATATGTCGC----GCC----------GCGCGCG

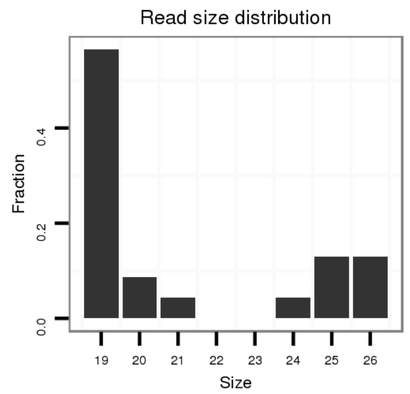
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_776	**2:24971703-24971774 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

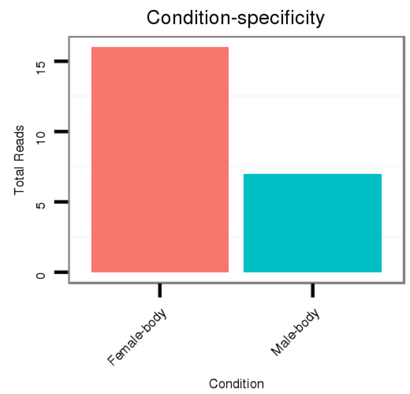
Legend: mature star mismatch in alignment mismatch in read

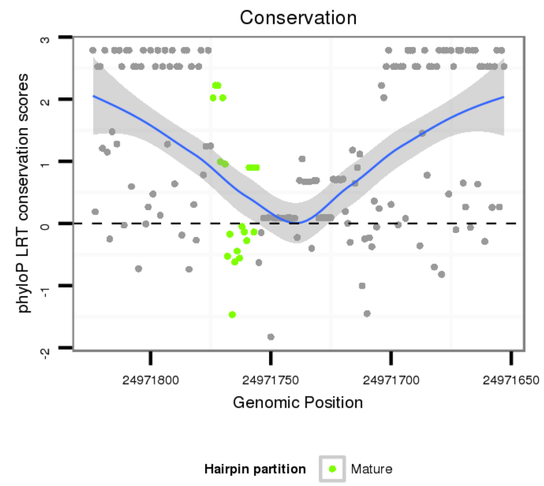
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA26267-in]; CDS [Dpse\GA26267-cds]; CDS [Dpse\GA26267-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATCCCACCTACTCGTTCCGTGAGCTGGTCGAGCAGGCTATTCTGCAAGTGGTAAGTGTGTGGAGATAGTCGCGATAGTGGGTTCCGTTCCGCTTGATTTATCACTCTTTATCACTCTTACAGGAAGGTGCCTTTGCCATTGCCGTGAAGTCCAAACACTTCCCCGGAGAGTG **********(((((.(((((((((.....(((((.....))))))).....))))))..))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M059 embryo
.....GTAAGTGTGTGGAGATAGT.....	19	0	1	12.00	12	8	4	0
.....GTAAGTGTGTGGAGATAGTCGCGATA.....	26	0	1	3.00	3	3	0	0
.....GTAAGTGTGTGGAGATAGTCGCGAT.....	25	0	1	3.00	3	2	1	0
.....CGTTCCGTGAGCTGGTCGAGC.....	21	0	1	2.00	2	2	0	0
.....GTGTGGAGATAGTCGCGATA.....	20	0	1	1.00	1	0	1	0
.....GGAAGGTGCCTTTGCCATTGC.....	21	0	1	1.00	1	1	0	0
.....GTAAGTGTGTGGAGATAGTC.....	20	0	1	1.00	1	1	0	0
.....GTAAGTGTGTGGAGATAGTCGCGA.....	24	0	1	1.00	1	0	1	0
.....AACACTTCCCCGGAGAGT.	18	0	1	1.00	1	1	0	0
.....GTAAGTGTGTGGAGATAGTCG.....	21	0	1	1.00	1	1	0	0
ATCCCACCTACTCGTTCCGTGAGCTG.....	26	0	1	1.00	1	1	0	0
.....AAGTCCAAACACTTCCCCGGAGA...	23	0	1	1.00	1	1	0	0
....CACCTACTCGTTCCGTGAGCTG.....	22	0	1	1.00	1	1	0	0
.....CGTGAGCTGGTCGAGCAGGCTATTCTGC.....	28	0	1	1.00	1	1	0	0
.....AGTCCAAACACTTCCCCGGAGAGT.	24	0	1	1.00	1	1	0	0
.....CTACTCGTTCCGTGAGCTGGTC.....	22	0	1	1.00	1	1	0	0
.....GTAAGTGTGTGGAGATAGTCGCGAC.....	25	1	1	1.00	1	1	0	0
.....GTGAGCTGGTCGAGCAGG.....	18	0	1	1.00	1	1	0	0
.....TGTGGAGATAGTCGCGATA.....	19	0	1	1.00	1	1	0	0

Anti-sense strand reads

TAGGGTGGATGAGCAAGGCACTCGACCAGCTCGTCCGATAAGACGTTCACCATTCACACACCTCTATCAGCGCTATCACCCAAGGCAAGGCGAACTAAATAGTGAGAAATAGTGAGAATGTCCTTCCACGGAAACGGTAACGGCACTTCAGGTTTGTGAAGGGGCCTCTCAC **********(((((.(((((((((.....(((((.....))))))).....))))))..))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR902012 CNS imaginal disc	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:24971653-24971824 -	dps_776	ATCCCACCTACTCGTTCCGTGAGCTGGTCGAGCAGGCTATTCTGCAAGTGGTAAGTGTGTGGA----------GATAGTCGCGATAGTGGGTTCCGTTCCGCTTGATTTATCACTCTTTA----------TCACTCTTACAGGAAGGTGCCTTTGCCATTGCCGTGAAGTCCAAACACTTCCCCGGAGAGTG
droPer2	scaffold_6:270342-270513 -	dpe_1866	ATCCCACCTACTCGTTCCGAGAACTGGTCGAGCAGGCTATTCTGCAAGTGGTAAGTGTGTGGA----------GATAGTCGCGACAGTGGGTTCCGTTCCGCTTGATTTATCACTCTTTA----------TCACTCTTACAGGAAGGTGCCTTTGCCATTGCCGTGAAGTCCAAACACTTCCCCGGAGAGTG
droWil2	scf2_1100000004943:13604433-13604603 -		ATCCAAATTACTCGTTCCGCGAACTCGTCGAGCAGGCATTCTACAAGTGGTAAGTGCATTTA----------ACTGA----------TAGGCGGTTATCAGGCTACTA----AGCA-CTTA----------A-----------ATTCCGATT----------GCTG--AT-----TACTTACAGGAAGGCGCATTTGCCATTGCCGTAAAGTCCAAGTATTTCCCCGGTGAATG
droVir3	scaffold_13047:13614705-13614885 +	dvi_16838	ATCCCAACTACTCGTTCCGTGAGCTGGTCGAGCAGGCATACAGCAAGTGGTAAGTAACCC-ATTGAT-GTG-AAAACCAAGGTTCATTAT----------G----AGCA-CTTGATTATGT---GGCTATATTCG----------TG-T----------TTCCTGTTTAAAGGAGGGTGCATTTGCAATTGCTGTAAATTCGAAGCATTTCCCAGGCGAGTG
droMoj3	scaffold_6540:10860849-10861032 +		ATCCCAACTACTCGTTCCGCGAGCTCGTCGAGCAGGCCATTCTGCAAGTGGTAAGTGAGTCCACTCAG-GTG-GAAACCGAATCTCATTAT----------GTTATAGAATCCTCATGATGTGT----------T----------TCACTTG-T----------TTCGTGCTGACAGGAAGGCGCATTTGCCATTGCAGTTAAATTCGAAGCATTTCCCGGCGAGTG
droGri2	scaffold_15074:401940-402113 -		ATCCCAACTACTCGTTCCGCGAACTGGTCGAGCAGGCCATACAACAAGTGGTAAGTTAATTCA----------AAACCTAACCTTATTAAGGACAAACT----------CTTATTGATGTCATGACTTTAATTGA----------T----------TTT---GTTTGTAGGAGGGCGCATTTGCCATTGCTGTCAAGTCGAAGCATTTCCCGGCGAGTG
droAna3	scaffold_12911:1983818-1983981 +		ACCCCACCTACTCGTTTCGCGAGTTGGTCGAGCAAGCTATAGAGCAGTTGGTAAGTTTGCCCGA---T-GCT-AGAATTAAAGT----------TC----A----------CCACATTACACATATTCAAAAAT---CATTCGCGAGGAAGGTGCTTTGCAGTCGCTGTAAATTCAAGTATTTTCCTGGCGAGTG
droBip1	scf7180000396714:1067973-1068136 -		ACCCCACCTACTCCTTTCGCGAGTTGGTTAGAGCAGGCTATAGAGCAGTTGGTAAGATTGACCTA---T-GAG-AGCATTGAAGT----------TA----A----------ACACATTGAACTTATCCCAAAAC---CGTACGCAGGAAGGCGCATTTGCAGTCGCTGTCAAGTCAAAGTATTTCCCTGGAGAGTG
droKik1	scf7180000302297:46177-46331 -		ACCCCACATACTCGTTCCGCGAGTTGGTCGAGCAGGCTATTCTGCAAGTGGTAAGTGGTCCCAATGGA-GTG-T----------CTATACCACCTAAAATC--GGCCC--TT---CTCCTACAGGAAGGCGCATTTGCCATTGCCGTGAAGTCAAGCACTTCCCCGGAGAGTG
droFic1	scf7180000454068:15701-15862 -		ACCCCACCTATTCGTTCCGCGAGCTGGTCGAGCAGGCCATCCTTCAAGTGGTATGTTGTCCA-C---GGTATCAGCCGTGCAG----------CA----A----------CCAACTAAATTT--TGCAAACCC---CCTGTGCAGGAAGGCGCTTTGCTATCGCTGTGAAGTCCAAGCACTTTCCCGGAGATG
droEle1	scf7180000491278:33183-33345 +		ACCCCACGTACTCATTCCGCGAGCTGGTCGAGCAGGCCATCCTTCAAGTGGTAAGTTGTTTT-T---TGTCGTAGCTAA----------GGAGCAACTCTCAG-TCAGTG----A----------CCACCTGAAA----------TTTGCAGGAAGGCGCCTTTGCTATTGCGTGAAGTCCAAGCACTTTCCTGGAGAGTG
droRho1	scf7180000775729:3799-3959 +		ACCCCACATACTCGTTCCGCGAGCTGGTCGAGCAGGCCATCCTTCAAGTGGTAAGTTGCCTCT----GGGCGCAGCTAT-ATAG----------TC----A----------CCACCTAAAATGTA----ATAAT-C-GTTGTGGAGGAAGGCGCCTTTGCCATTGCGTGAAGTCCAAGCACTTTCCCGGAGAGTG
droBia1	scf7180000301256:49076-49175 +		ATCCCACATACTCGTTTCGTGAACTGGTCGAGCAGGCCATTCTCCAAGTG----------GAAGGCGCCTTTGCCATTGCCGTGAAGTCCAAGCATTTTCCCGGAGAGTG
droTak1	scf7180000410621:31069-31168 -		ATCCCACCTACTCGTTTCGCGAGCTGGTCGAGCAGGCCATCCTCCAAGTG----------GAAGGCGCCTTTGCCATTGCCGTGAAGTCCAAGCATTTTCCCGGAGAGTG
droEug1	scf7180000409540:3761-3860 +		ACCCCACCCACTCTTTCCGCGAGTTGGTTGAACAGGCTATCCTCGAGGTT----------GAAGGCGCCTTTGCTATTGCTGTGAAGTCCAAGCATTTTCCTGGAGAATG
dm3	chr3RHet:2477494-2477593 +		ACCCCACCTACTCCTTCCGCGAGCTGGTCGAGCAAGCCATCCTTCAAGTG----------GAGGGCGCCTTTGCTATTGCCGTAAAGTCAAAATACTTTCCCGGAGAGTG
droSim2	21:22493057-22493156 -		ACCCCACCTACTCGTTCCGCGAGCTGGTCGAGCAAGCCATCCTTCAAGTG----------GAGGGCGCCTTTGCTATTGCCGTAAAGTCCAAATACTTTCCCGGAGAGTG
droSec2	scaffold_6:105530-105629 +		ACCCCACCTACTCGTTCCGCGAGCTGGTCGAGCAAGCCATCCTTCAAGTG----------GAGGGCGCCTTTGCTATTGCCGTAAAGTCCAAATACTTTCCCGGAGAGTG
droYak3	3R:327480-327579 +		ATCCCACCTACTCGTTCCGCGAGCTGGTCGAGCAAGCCATCCTTCAAGTG----------GAGGGCGCCTTTGCTATTGCCGTAAAGTCCAAGTACTTTCCCGGAGAGTG
droEre2	scaffold_4770:334345-334444 +		ACCCCACCTACTCGTTCCGCGAGCTGGTCGAGCAAGCCATACTTCAAGTG----------GAGGGCGCCTTTGCTATTGCCGTAAAGTCCAAGTACTTTCCCGGAGAGTG

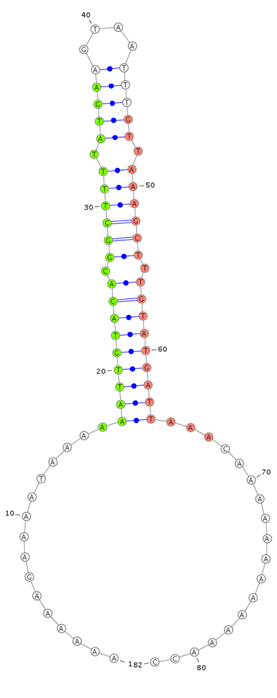
Generated: 09/08/2015 at 07:06 PM

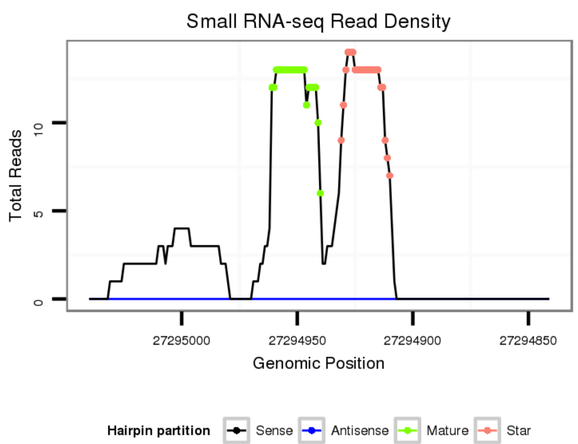
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

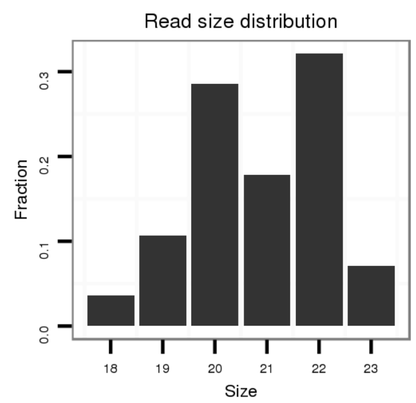
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3827	**2:27294891-27294990 -**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

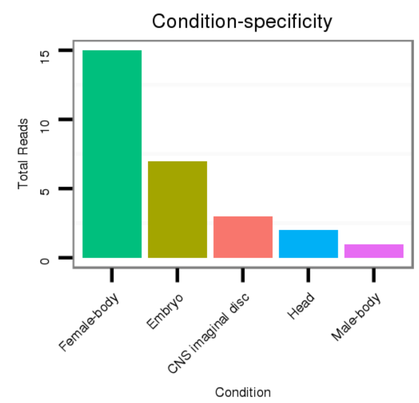
Legend: mature star mismatch in alignment mismatch in read

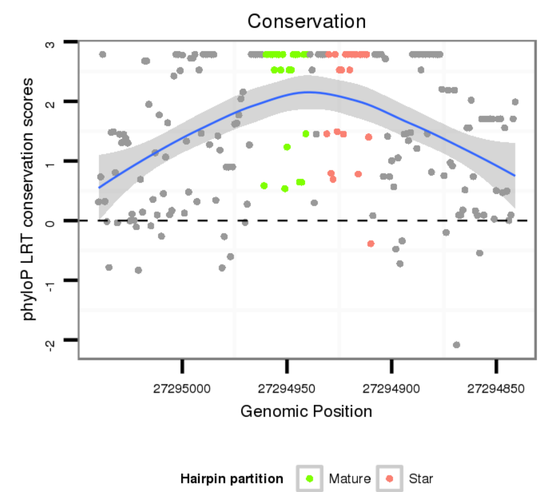
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
T-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAACAAAAGAAAAACCCTTACAAACCAAATCCATTCAACAGAAAAAACAATAGAAGAACAAAAAAAAAAGAAAATAAAAAATTGTACACGGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATGATTAAACAAAAAAAAAAACCAAATTTGTGTTTTTATTTGCATTTTTTACCCGTTTACTTTTTTAGTTGGCGATT **********.....(((((((((.(((((((.(((((....)))))).)))))))..)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo	M059 embryo	SRR902012 CNS imaginal disc	GSM444067 head	M062 head	V112 male body
.....AAATTGTACACGGCTTTTATGA.....	22	0	1	3.00	3	1	0	1	1	0	0	0
.....AAATTGTACACGGCTTTTATG.....	21	0	1	3.00	3	3	0	0	0	0	0	0
.....AAGCTTTGTATGATTAAACT.....	20	1	1	2.00	2	2	0	0	0	0	0	0
.....AAATTGTACACGGCTTTTAT.....	20	0	1	2.00	2	2	0	0	0	0	0	0
.....GTTAAAGCTTTGTATGATTAAA.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....TGTTAAAGCTTTGTATGATT.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....TACACGGCTTTTATGAAGTAATTTGC.....	26	1	1	1.00	1	0	0	1	0	0	0	0
.....TCCATTCAACAGAAAAAACAATAGAAG.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....GAAAAACCCTTACAAACCAAATCC.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....TTTTATGAAGTAATTTGTTA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TTCAACAGAAAAAACAATAGAAGAACA.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....AAAATAAAAAATTGTACACGGC.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....TTAAAGCTTTGTATGATTAAAC.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....TTATGAAGTAATTTGTTAAA.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....CCCTTACAAACCAAATCCATTCAACAGAA.....	29	0	1	1.00	1	1	0	0	0	0	0	0
.....AAAATTGTACACGGCTTTTATG.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....TTAAAGCTTTGTATGATTAAACA.....	23	0	1	1.00	1	0	0	0	1	0	0	0
.....TAAAGCTTTGTATGATTAA.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....AAGCTTTGTATGATTAAAC.....	19	0	1	1.00	1	0	0	0	0	1	0	0
.....TAATTTGTTAAAGCTTTGTATGA.....	23	0	1	1.00	1	0	1	0	0	0	0	0
.....AACAGAAAAAACAATAGAAGAAC.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....TTAAAGCTTTGTATGATTT.....	19	1	1	1.00	1	1	0	0	0	0	0	0
.....TTTGTTAAAGCTTTGTATGATT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....ATTGTACACGGCTTTTATGA.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....AAAGCTTTGTATGATTAAA.....	19	0	1	1.00	1	0	1	0	0	0	0	0
.....TTGTTAAAGCTTTGTATGATT.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....ATAAAAAATTGTACACGGCT.....	20	0	1	1.00	1	0	0	0	0	1	0	0
.....AAAAAATTGTACACGGCT.....	18	0	1	1.00	1	0	1	0	0	0	0	0
.....GTTAAAGCTTTGTATGATTA.....	20	0	1	1.00	1	0	0	0	0	0	0	1
.....TAAAGCTTTGTATGATTAAAC.....	21	0	1	1.00	1	0	0	0	1	0	0	0

Anti-sense strand reads

TTTTGTTTTCTTTTTGGGAATGTTTGGTTTAGGTAAGTTGTCTTTTTTGTTATCTTCTTGTTTTTTTTTCTTTTATTTTTTAACATGTGCCGAAAATACTTCATTAAACAATTTCGAAACATACTAATTTGTTTTTTTTTTTGGTTTAAACACAAAAATAAACGTAAAAAATGGGCAAATGAAAAAATCAACCGCTAA **********.....(((((((((.(((((((.(((((....)))))).)))))))..)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	M022 male body	GSM343916 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:27294841-27295040 -	dps_3827	AAAAC---A-AAAGAA--------AAACCCTTACAAA----------CCAAATC---CATTCAA-CAG--AAA------AAACAATAGAAGAA-CAAAAA-AAAAAGAAAATAAA-AAATTGTACACGGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATGATTAAACAAAAAAAAA--AAA-CCAAA-TTTGTGTTTTTATTTGCATTTTTTACCCGTTTACTTTTTTAGTTGGCGATT
droPer2	scaffold_6:2585040-2585241 -	dpe_2481	AAAAC---A-AAAGAA--------AAACCCTTACAAA----------CCAAATC---CATTCAA-CAG--AAA------AAACAATAGAAGAA-CAAAAA-AAAAAGAAAATAAA-AAATTGTACACGGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATGATTAAACAAAAAAAAAAACC-CCAAA-TTTGTGTTTTTATTTGCATTTTGTAACCGTTTACTTTTTTAGTTGGCGATT
droWil2	scf2_1100000004902:4649898-4650075 +	dwi_5415	AAAAATA-CAAAAAA--------AAACCAAAACAAA-----AGAAAAGAAAAGTTTAAAAAATCAAAACAACC----------AACCAACCA--ACA------AAACAATAGAAA--------AATAAA-CAATTGTACACGGCTTTTATAAAGTAATTTATTAAAGCTTTGTATAATTACCCAAAAAAAAAACCC-AAAAA-TTTTGTTTTTATTTG----------
droVir3	scaffold_13047:1835007-1835158 +	dvi_24634	TGAGC---A-AAAAGA--------G----------AACAA--CCCAACCAACA--A------AAACAATAGAAAA-AAAACATAAAAAAAAATAAAAAATTGTACACGGCTTTCGAAAGAAATTTATTGAAGCTTTGTATAATTACAAAAAAAA--AACCTTGAAC-TTTGTGTTTTTATTT----------
droMoj3	scaffold_6540:3761878-3762073 +	dmo_3126	AAAAA---A-AAAAAAAA------AA--GAAACAAA-----ATGAAAGAAAG----A----------AGAGATGAA--CCCAACCAACAACAAAAAAAACCAATAGAAAAAGTAAAA-AAAAAAAAAATAAA-CAATTGTACACTGCTTTCGAAAGAAATTTATTGAAGCTTTGTATAATTAAAAAAAAAAA--AAC-TGACTTTTGTGTTTTTATTTGATTTAT---T---TAC----------
droGri2	scaffold_14906:8668123-8668298 +	dgr_462	AAAGAGC-GAAAAGAA--------AA--TACGAAAAACTAAAAAAAAAAAAA----------AGTG--AACAA--CCCAACCA--ACA------AAACAATAGAAA--------AAAATAAA-CAATTGTACACGGCTTTCGAAAGAAATTTATCGAAGCTTTGTATAATTAACCAAAAAAAAACAACC-TGATC-TTTGTGTTATTATTTGCTTTAT----------
droAna3	scaffold_13340:11049297-11049444 -	dan_90	AGAAA---A-AAAAAC--------AAATATTTGAAAA----------AGAAATCAACC-CTCAACCAACCACA------AAGCAATAGAAA--------AAATAAA-CAATTGTACACGGCTTTCGAAAGTGATTTATTAAAGCTTTGTATAATTAAGAAAACAA--------CAAA-TTTGTGTTTTTATTT----------
droBip1	scf7180000396374:34247-34385 +		GAAAA---G-AAAAAA--------AA------ACAAA----------AGAAATC---C-CTCAACCAACCACA------AAGCAATAGAAA--------AAATAAA-CAATTGTACACGGCTTTCGAAAGTGATTTATTAAAGCTTTGTATAATTAACAAAACAA--------CAAA-TTTGTGTTTTTATTT----------
droKik1	scf7180000302247:250335-250522 +		AAAACAA-CTAAAGA--------AA--CCCCACAA----------AACC-----AACCAACCATCAACA------AAACAATAGAAGAA-A-----AAAAACAAAATAAA-CAATTGTACATGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAACAC--AAC-CAAAA-TTTGTGTTTTTATTTGCCTTAT---CACGTACACT-TTTTCGTTGGCGATT
droFic1	scf7180000454106:2527562-2527743 +		AAAACC-C-G-AAAGAA--------AA--CCCCACAA----------AGCC--AAC---C-ACCAACCACCACA------AAACAATAGAAA--------AACAAATAAA-CAATTGTACACGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA--AACC-TCCAA-ATTGTGTTTTTATTTGCCTTAT---CACGTACCAT-TTTTCGTTTGTAATT
droEle1	scf7180000491212:1154162-1154341 +		AAAAATA-G-AAAGAA--------AA--ACCCACAA----------AACC--ATC---C-ACCAACCAGC-------------AACAATAAAAA--------AAACAAATAAA-CAATTGTACACGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAGA--AACC-CCAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTAAAAT-TTTTCGTTGGCATTT
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droTak1	scf7180000414009:179067-179247 +		AAAAAAAACG-AAAGAA--------AA--CCCTAAAAA----------AACC-----AACCAACCAACAAGA------AAACAATAGAAA--------AAACAAATAAA-CAATTGTACACGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAAA-----AACC-TCAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTACAAT-TTTTCGTTGGCCATT
droEug1	scf7180000409490:80938-81127 +		GAAGA---A-GATGAAAAAACGAAAT--CCCCCACAA----------AACC-----AACCAACCAACAACA------AAACAATAGAAA--------AAAAATCAAATAAA-CAATTGTACATGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA--AACC-TCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTTGGCAATT
dm3	chr3R:4640227-4640405 -	dme_421	AAAAA---G-AAAGAA--------AA--CCCCACAAA----------CC-----AAACAA-CAACAACA------AAACAATAGAAA--------AAAGAAATAAA-CAATTGTACATGGCTTTCGAAAGAATTTATGAAGCTTTGTATGATTAACCAAAAAAAA-ATCC-ACAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTACAGT-TTTTCGTTGGCACTT
droSim2	3r:16351723-16351906 +	dsi_75	AAAAA---G-AAAGAA--------AA--CCCCACAAA----------CC-----AAACAAC---AACAACAACAAAACAATAGAAA--------AAAAACAAATAAA-CAATTGTACATGGCTTTCGAAAGAATTTATTAAAGCTTTGTATGATTAACCAAAAAAAA--TCC-TGAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTACAGT-TTTTCGTTGGCAATT
droSec2	scaffold_0:17217371-17217550 +	dse_1844	AAAAA---G-AAAGAA--------AA--CCCCACAAA----------CC-----AAACAA-CAACAACA------AAACAATAGAAA--------AAAAACAAATAAA-CAATTGTACATGGCTTTCGAAAGAATTTATTAAAGCTTTGTATGATTAACCAAAAAAAA--TTC-TGAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTACAGT-TTTTCATTGGCAATT
droYak3	3R:8702161-8702341 -	dya_1796	AAAAA---G-AAAGAA--------AAA-CCCGTCAAA----------CC-----AAACAACAACA------AAACAATAGAAGA--------AAAAACAAATAAA-CAATTGTACATGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAAA-ATCC-TCAAA-TTTGTGTTTTCATTTGCGTTAT---CACGTACAGT-TTTTCGTTGGCAATT
droEre2	scaffold_4770:16945893-16946068 +	der_1521	AAAAA---GAAGAAAA--------AA--CCCCACAAA----------G------AAACAACAACA------AAACAATAGAAA--------AAAACAAATAAA-CAATTGTACATGGCTTTCGAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAA--TCC-TCAAA-TTTGTGTTTTTATTTGCGTTAT---CACGTACAGT-TTTTCGTTGGCAATT

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	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	0
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	8
rescue.candidate	4

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
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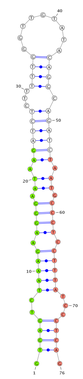
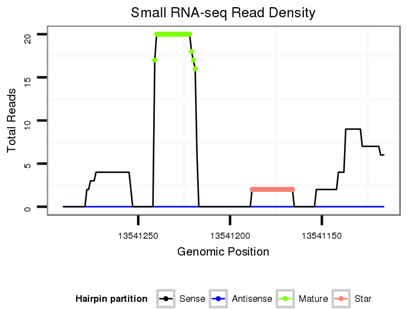
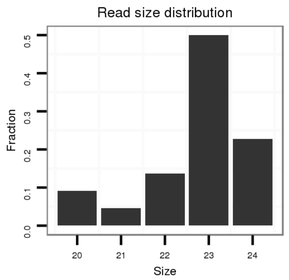
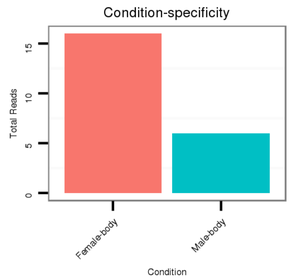
Legend: mature star mismatch in alignment mismatch in read

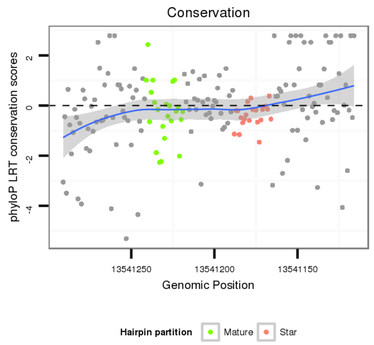
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dpse\GA22127-in]; intron [Dpse\GA15887-in]; CDS [Dpse\GA15887-cds]; CDS [Dpse\GA15887-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TTACCCAAAGAGGGTAGCCAGGAGATTGAAATGAAGGAGTTGTTGTTAACGTGAGTCTAAAGAAGGGAATAAGATCTCTTTTTGGGTTGTATACAGGCAGATCTAATGCCCTCCTTTATCCCTCAGGTATGCTGTGGATATCATTGCCTCGACCATCTTTGGCCTGGATGTGGACA
**************************************************.((((..(((((.((((.((.((((((...(((((.........))))..))))))..))..)))))..))))))...)))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM444067 head	M059 male body	GSM343916 head	embryo	embryo
23	0	1	8.00	8	6	2	0	0	0		
24	0	1	5.00	5	4	1	0	0	0		
24	1	1	5.00	5	3	1	1	0	0		
22	0	1	4.00	4	3	1	0	0	0		
20	0	1	2.00	2	1	1	0	0	0		
23	1	1	2.00	2	2	0	0	0	0		
22	0	1	2.00	2	2	0	0	0	0		
19	0	1	1.00	1	1	0	0	0	0		
23	0	1	1.00	1	1	0	0	0	0		
22	0	1	1.00	1	0	1	0	0	0		
22	0	1	1.00	1	1	0	0	0	0		
21	0	1	1.00	1	0	1	0	0	0		
19	0	1	1.00	1	1	0	0	0	0		
21	0	2	0.50	1	1	0	0	0	0		

Anti-sense strand reads

```
AATGGGTTTCTCCCATCGGTCCTCTAACTTTACTTCCTCAACAACAATTGCACTCAGATTTCTTCCCTTATTCTAGAGAAAAACCCAACATATGTCCGTCTAGATTACGGGAGGAAATAGGGAGTCCATACGACACCTATAGTAACGGAGCTGGTAGAAACCGGACCTACACCTGT
**************************************************.((((..(((((.((((.((.((((((...(((((.........))))..))))))..))..)))))..))))))...)))))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	V112 male body	GSM444067 head	M022 male body	M062 head	GSM343916 embryo

Show Alignment With Reads

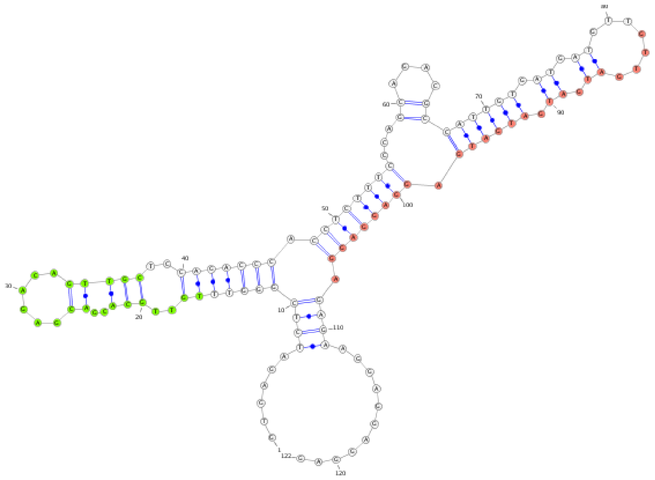
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:13541116-13541291 -	dps_522	TTACCCA----------AAGAGGGTAGCCA-GGAGATTGAAATGA-AGGAGTTGTTGTTAACGTGAGTCTAAAGAAG--G----------GA----------ATAAGAT----------CTCTTTTTGGGTTGTATACAGG----------CAGATCTAATGCC----------CTCCTTT----------ATCCCTCAGGTATGCTGTGGATATCATTGCCTCGACCATCTTTGGCCTGGATGTGGACA
droPer2	scaffold_0:6908473-6908648 +	dpe_420	TTACCCA----------AAGAGGGTAGCCA-GGAGATTGAAATGA-AGGAGTTGTTGTTAACGTGAGTCTAAAGAAG--G----------GA----------ATCAGAT----------CTCTTTTTGGTTGTATACAGG----------CAGATCTAATACC----------CTCCTTT----------ATCCCTCAGGTATGCTGTGGATATCATTGCCTCGACCATCTTTGGCCTGGATGTGGACA
droWil2	scf2_1100000004921:1996138-1996302 +		TTGCCAG----------AGGATGGTAGCAA-GGAGATTGATTA-AGGATTATTAACCACGTGAGTGTCCAG--T----------GA----------ATTCAATCTATTGAAT-----TTGTTTGCA----------T----------C-CAAGA--T----------TGA----------TTCTC-TTTTCAGCTATGCCATCGATCATAGTTCGACCATTTTGGCCTGGATGTGA
droVir3	scaffold_12822:3647853-3648029 +		ATACAGC----------AGTCGGCGATGT-GGAATTGATCTATA-AGATTTGATGTCATGTGTAGTGTTAGCTGTCAC-TTTC----------------------CATGTAGT--ATTTCATGCTTAGATAATTGC--TGCCTTCT----C-----CGTTTGC-TATTTGAGCTTGTGATTGATATTGGCCTCGACCATTTTGGCCTGGATGTGGACA
droMoj3	scaffold_6540:16962620-16962783 +		CTACAGC----------AGTCATGCGGCAACTTGAATTGATATGA-AGATTTAATGCCTGTGTAAGCAACTGTT---TGTC----------------------G----------AATACCTATCT----TCATG----------AGATCCTTCATT----------TCCCCAT----------TGCTTTCAGCTATGCTGATTGATATCATTGCCTCGACTATACTTGGTTGGATGTGGACA
droGri2	scaffold_14906:1255381-1255552 +		ATCCAGC----------GGTCATGCTCTGTTATGATGTGATATGA-AGATTTGATGTCATCTTAGCAATTTTT-AA-AATTACACACATTTAC--------------------------TGGAT-----ATATATGTA----------TTTTCCGGCT----------GAACTGT-TTTTCAGCTATGCTGATATTGATTGCCTCGACCATATTTGGCCTTGATGTGGACA
droAna3	GTTCCAA----------AATAGATAGCATTTAGTTGTGATATGA-AGGCCTGATGTCCACTAAGTCGTGGCAA--T----------------------TCTTTTCA-CTCCAA--TAT----------TTATCTAAGA--T----------CTATTT----------TATGTATATGCCATCGATATCATGCCTCACCATTTTGGACTTGATGTGGACA
droBip1	scf7180000396413:1781985-1782139 +		CTGCCCG----------AAAGGGCGAGCAA-GGAAGTTGAAATTA-AGGAACTTTTCCCACGTGAGTCATGAT--T----------------------TCTTTC--AAT----------ATTGGA---AC-CAAAA--T----------AC-----ACTCGT-TCTCTAGTATGCTGTGATGTCATTGCCTCGACCATTTTGGGCCTGGATGTGGACA
droKik1	scf7180000302634:848696-848902 -		GAATCTG--------AGCCGTCCCGCGGCAA-GGAAGTTGAATGA-AGATGGCATGTCAACCTGAGTTGGCGGAAAA-T----------------------T----------CTTGATT----------CTCTCAGTGCACCCTGGAAATTTGTTTATCTCTGGAACGTAAATTTCAATTATATTTGGTTTTATTCGTTCCTCCTAGTTAGCGATATAGTTGCCTCGACTATTTTGGCCTGGATGTGACA
droFic1	scf7180000454055:301018-301117 -		CTCCCAG----------AAGATGGTTTTAA-GGAGATGATCTCA-AGAAAGTGATGCAG----------T----------T----------T

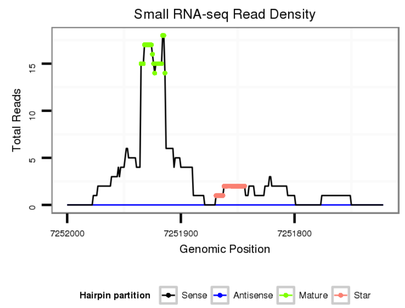
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3825	**2:7251772-7251950 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

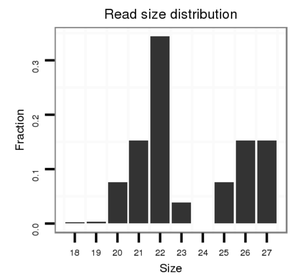
Legend: mature star mismatch in alignment mismatch in read

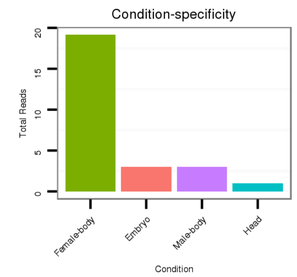
Predicted structure

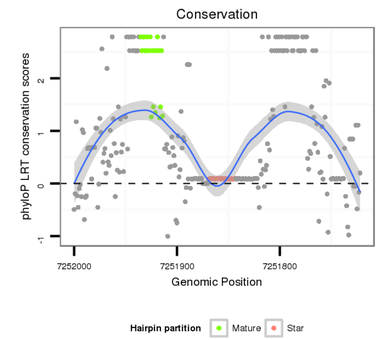


dps_3825_annot [-32.7]









Show Alternate Folds

Flybase annnotation

intron [Dpse\GA14324-in]

Repeatable elements

Name	Class	Family	Strand
(TCC)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGAGAGAGTGTACGAGAGTATATCTAATCTATAGAGTTTTCCATGCGTCAGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTCCAGACCCACCTCTTTCCCAGCAGACGCCATTGTGATGATGTTGTTGATGATGATGATGAGGAGGAGGAGAGAAGGAGGAGGGAGGGCTTATCCACTTGCAAACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGCCATTAACCATTGGAACCACTACGAATACAAATATATATACA	Read # size	Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM343916 embryo	M059 embryo	V112 male body	GSM444067 head	SRR902011 testis
**********	22	0	1	8.00	8	5	2	0	0	1	0
TGTTGCACGACGAGACAGTTGC	21	0	1	4.00	4	3	0	0	1	0	0
TGTTGCACGACGAGACAGTTG	27	0	1	3.00	3	3	0	0	0	0	0
TGCTCCAGACCCACCTCTTTCCCAGCA	26	0	1	2.00	2	2	0	0	0	0	0
TGCACGACGAGACAGTTGCTCCAGAC	26	0	1	1.00	1	1	0	0	0	0	0
GTTGATGATGATGATGAGGAGGAGGA	22	1	1	1.00	1	0	0	0	1	0	0
TGTTGCACGACGAGACAGTTGG	26	0	1	1.00	1	1	0	0	0	0	0
CACCTCTTTCCCAGCAGACGCCATTG	25	0	1	1.00	1	1	0	0	0	0	0
GAGATCTCGGGTTTGTTGCACGACG	26	0	1	1.00	1	1	0	0	0	0	0
CTTGTCAACGACGCCATTAACCATTG	28	0	1	1.00	1	1	0	0	0	0	0
TCAGTGAGATCTCGGGTTTGTTGCACGA	23	0	1	1.00	1	0	0	1	0	0	0
TCCACTTGCAAACGCAGCTGTCT	20	0	1	1.00	1	0	0	0	1	0	0
AAGGAGGAGGAGGGCTTATC	27	0	1	1.00	1	0	0	0	1	0	0
ATGATGATGAGGAGGAGAGAAGGA	21	1	1	1.00	1	0	0	0	1	0	0
CACTTGCAAACGCAGCTGTC	22	0	1	1.00	1	1	0	0	0	0	0
TCCATGCGTCAGTGAGATCTCG	27	0	1	1.00	1	1	0	0	0	0	0
TCTATAGAGTTTTCCATGCGTCAGTGA	20	0	1	1.00	1	1	0	0	0	0	0
CTTATCCACTTGCAAACGCA	25	0	1	1.00	1	1	0	0	0	0	0
TGAGATCTCGGGTTTGTTGCACGAC	23	0	1	1.00	1	0	0	1	0	0	0
CTAATCTATAGAGTTTTCCATGC	20	0	1	1.00	1	0	1	0	0	0	0
CGTCAGTGAGATCTCGGGTT	22	0	1	1.00	1	1	0	0	0	0	0
GACAGTTGCTCCAGACCCACCT	19	0	12	0.08	1	1	0	0	0	0	0
ATGATGATGATGAGGAGGA	18	0	14	0.07	1	1	0	0	0	0	0
GATGATGATGAGGAGGAG											

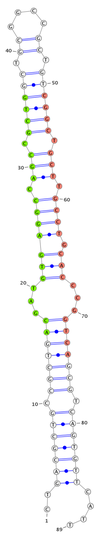
Anti-sense strand reads

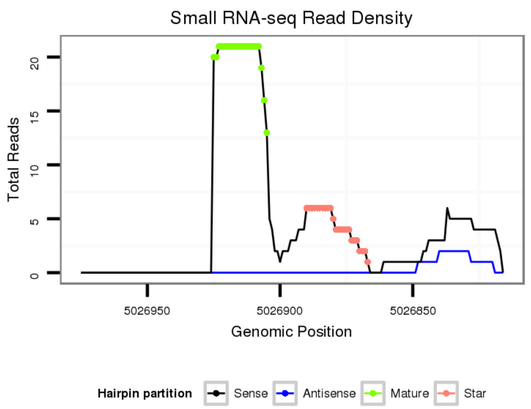
GCTCTCTCACATGCTCTCATATAGATTAGATATCTCAAAAGGTACGCAGTCACTCTAGAGCCCAAACAACGTGCTGCTCTGTCAACGAGGTCTGGGTGGAGAAAGGGTCGTCTGCGGTAACACTACTACAACAACTACTACTACTCCTCCTCCTCTTCCTCCTCCTCCCGAATAGGTGAACGTTTGCGTCGACAGAGAGCAACAAAAGCTAAAGCCCTAGAACAGTTGCTGCGGTAATTGGTAACCTTGGTGATGCTTATGTTTATATATATGT	Read # size	Mismatch	Hit Count	Total Norm	Total	GSM343916 embryo	M040 female body
**********	25	0	1	1.00	1	1	0
C-GA--------GAGAGTGTACGAGAGTATATC----------TAATCTATAGAGTTTTCCATGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTCCAGACCC---ACC---T----------CT---TT----------C-CCA-GCAGACGCCATTGTGATGATGTTGTTGATGATGATGAGGAGGAGGAGAGAAGGAGGAGGGAGGGCTTATCCACTTG--CAAACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGCC--ATT----AA----------C---------CA-TTG----GAACCACTACGAA----------TACAAATATATATACA	22	0	1	8.00	8	5	2
C-GA--------GAGAGTGTACGAGAGTATATC----------TAATCTATAGAGTTTTCCATGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTCCAGACCC---ACC---T----------CT---TT----------C-CCA-GCAGACGCCATTGTGAT-----GTTGATGATGATGAGGAGGAGGAGAGAAGGAGGAGGGAGGGCTTATCCACTTG--CAAACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGCC--ATT----AA----------C---------CA-TTG----GAACCACTACGAA----------TACCAATATATATACA	21	0	1	4.00	4	3	0
droWil2	scf2_1100000004902:91557-91733 -	dwi_5414	4-M--------H----------H----------F----------FGC-CAAGCGTGCTAAAGATCTCGGGTTTGTTGCACGACGAGACAGCCGCTAAACCCC--A-CTT-T--GCCACACCCTCT--TTGC---AA----------TGGTAAATACTCCC-TTTCTGAA-A----------TG-TATATTTAGGCGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTATTTACGAC-A---------T----------T---------T--T--------GTGAAC------TA--TT----------	27	0	1	3.00	3	3	0
droVir3	scaffold_13047:936854-937016 -	dvi_125	C-AA--------G----------H----------F----------FGAGTGC---TGTTTGAGAGACAAGTGTGATGATCTCGGGTTTGTTGCACGACGAGCCAGCTGCTCCAAA---T---T---T----------GCCAAA---TA----------T---T---T----------T-CA-TAATAGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGCTGCAGCAACGTG--ATG----T-------CCAAGCATCCCGGCGCTGCACCA----------	26	0	1	2.00	2	2	0
droMoj3	scaffold_6540:4939671-4939838 -	dmo_129	C-AA--------G----------H----------F----------FGAGTGC---TGTTTGAGAAAAATATGTGATGATCTCGGGTTTGTTGCACGACGAGACAGCTGCTCCAGA---TAC----T----T----T

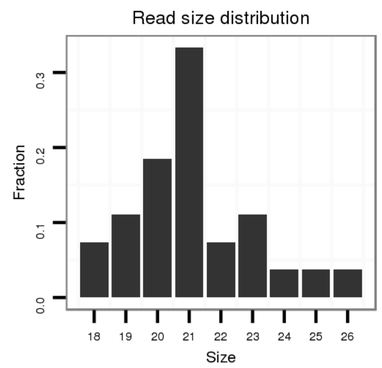
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_117	**2:5026866-5026925 -**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

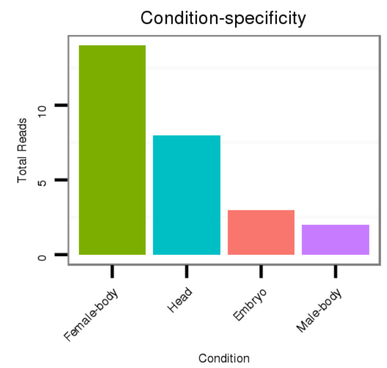
Legend: mature star mismatch in alignment mismatch in read

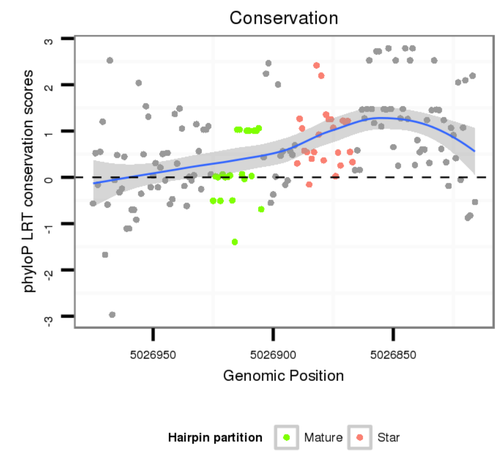
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGACGCTGGCGTCGTCGCCGTCGCCTTCTCTGCCGCTGACGCTGCCGCTGACGATGTGAGGCCAGCCGCTGGCTGCGGCCGCTGTCGGCTGCTTGCCTGCACCCGGTCAGCGTCAGTGTTCATTTCCCCATCGAGTCGGCCACACACGGGCAGGAGGCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	GSM444067 head	GSM343916 embryo	M062 head	V112 male body	M059 embryo
ACGATGTGAGGCCAGCCGCTG	21	0	1	8.00	8	3	2	0	2	1	0
ACGATGTGAGGCCAGCCGCT	20	0	1	3.00	3	1	2	0	0	0	0
ACGATGTGAGGCCAGCCGC	19	0	1	3.00	3	1	1	0	1	0	0
ACGATGTGAGGCCAGCCG	18	0	1	2.00	2	1	0	0	0	1	0
ACGATGTGAGGCCAGCCGCTGGC	23	0	1	2.00	2	1	0	0	0	0	1
GCCACACACGGGCAGGAGGCG	21	0	1	2.00	2	2	0	0	0	0	0
ACGATGTGAGGCCAGCCGCTT	21	1	1	2.00	2	0	2	0	0	0	0
CGGCTGCTTGCCTGCACCCGGTCA	24	0	1	1.00	1	1	0	0	0	0	0
GGCCGCTGTCGGCTGCTTGC	20	0	1	1.00	1	1	0	0	0	0	0
TGCGGCCGCTGTCGGCTGCTTG	22	0	1	1.00	1	1	0	0	0	0	0
GATGTGAGGCCAGCCGCTGGC	21	0	1	1.00	1	1	0	0	0	0	0
ACGATGTGAGGCCAGCCGCTGT	22	1	1	1.00	1	0	0	0	0	1	0
CGCTGTCGGCTGCTTGCCTGCACCCG	26	0	1	1.00	1	0	0	1	0	0	0
AGTGTTCATTTCCCCATCGAGTCGG	25	0	1	1.00	1	0	0	0	1	0	0
ACGATGTGAGGCCAGCCGCTGG	22	0	1	1.00	1	1	0	0	0	0	0
CGAGTCGGCCACACACGGGCAGGAGG	26	0	1	1.00	1	0	0	1	0	0	0
TGTCGGCTGCTTGCCTGCAC	20	0	1	1.00	1	1	0	0	0	0	0
ATCGAGTCGGCCACACACG	19	0	1	1.00	1	0	0	1	0	0	0
CGGCTGCTTGCCTGCACCCGGTC	23	0	1	1.00	1	0	0	0	0	0	1
ACGATGTGAGGCCAGCCGCTGGCTG	25	0	1	1.00	1	1	0	0	0	0	0
GCCACACACGGGCAGGAGGC	20	0	1	1.00	1	1	0	0	0	0	0
CGATGTGAGGCCAGCCGTAT	20	3	5	0.20	1	1	0	0	0	0	0

Anti-sense strand reads

GCTGCGACCGCAGCAGCGGCAGCGGAAGAGACGGCGACTGCGACGGCGACTGCTACACTCCGGTCGGCGACCGACGCCGGCGACAGCCGACGAACGGACGTGGGCCAGTCGCAGTCACAAGTAAAGGGGTAGCTCAGCCGGTGTGTGCCCGTCCTCCGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
AGCCGGTGTGTGCCCGTCCTC	21	0	1	1.00	1	1
GGTAGCTCAGCCGGTGTGTG	20	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:5026816-5026975 -	dps_117	CGACGCTGG------CG------TC----------GTCGC---CGTCGCCTTCTCTG-CCGCTG----A---CGCTGCCGCTGACGATGTGAGGCCAGCCGCTGGCT----------GCGGCCGC-------TG----------TCGGCTGCTTGCC--TGCA---------CC--CGG--------TCAGCG------TCAGTGTTCATTTCCCCATCGAGTCGGCCACACA--CGGGCA----------GGAGGCGT----------
droPer2	scaffold_19:732278-732437 -		CGACGCTGG------CG------TC----------GTCGC---CGTCGCCTTCTCTG-CCGCTG----C---CGCTGACGCTGACGATGTGAGGCCAGCCGCTGGCT----------GCGGCCGC-------TG----------TCGGCTGCTTGCC--TGCA---------CC--CGG--------TCAGCG------TCAGTGTTCATTTCCCCATCGAGTCGGCCACACA--CGGGCA----------GGAGGCGT----------
droWil2	scf2_1100000004902:11175864-11175987 -		TGACGTCGA------CT------TC----------G--GTTGCTCTG------GTG-GT---GC---TGGTGCTGCT----------GCTGCAGTTGCTGTTGGCG-TTTTGGCATTTGCT-T----------TGGTC-------+----------+---TGG--------CGACAG------TCAGTGTTAATTTCCTCATCGAGTTGGCAACACA--G-----+----------+--------
droVir3	scaffold_12855:2693621-2693788 -	dvi_106	CGCAGTGCG------TG------TC----------G----+----------GT-+-----GT---CGCAGTCGGA----------GCTGCAGTTGACGTCGAGCGCT------TGCGGCGTGCCCGT--TGGCTGCCAGCTGCCGTCTGCTTTCAGCTGCAACGGCCAACGT--CGTTCAGTCG-CGAGTC----GTCAGTTTTAATTTCCACATCGAGTTAACGACA-T--CACGAG----------+---GCG-+----------
droMoj3	scaffold_6540:11894784-11894934 -	dmo_261	CA-CGCTGT------CG------+----------+-----+---+----------GT-+-----GT---CGCTAGCGGA----------GCTGCAGTCAGCGCTGGCA-----+------+---GCGCTGCCTGTGCTGGCTGCCAGTTGCCGTATGCTTTGAGCTGCAACGGCCAACGT--CGG--------CAGTCG------TCAGTTTTAATTTCCACATCGAGTTAACGACA-T--CACG--+----------+-AAGCGG-+----------
droGri2	scaffold_14624:2256914-2257090 +		TGACGTCGG------CA------CGCT----------GTTC---TGTTGCGTTGGTGAGAGCTG----C---TGCTGCTGCTAGCTGCTTGCTGCTTGCCGCTAGCT----------GCTTGGGCTGC------AT----------TGAGG--------+---TGCAACAGCC---AA--CGGGCAA-CGTCAGTCG------TCAGTTTTAATTTCCACATCGAGTTAACGAACACA--CGAGAG---GCGGCA---GCAGCAG-+----------
droAna3	scaffold_13340:6482871-6483053 +		CGTGCACGA------CG------TCGATGTGGCTGCCGCTGCCAC---CGCTGCTGTTGCCA-GTGCTG----C---TGCTGCTGCTGCTTCCTGCAGAGCGT----------+----TCTGCTGCTTTGGTTGC------TG----------TTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCG------TCAGTGTTCATTTTCCCATCGAGTCAACAGCACACACGGTCAGGAGCGGCCAGGAAGGAGT----------
droBip1	scf7180000396708:2366141-2366292 -		CGCTGCAGT------CGACGACGCCG----------ACGTC---TG---------GT-+--GCTA---C---GGGTAGTGCTGCGCTGCAGCGCCT----------+----TCTGCTGCTTTGGTTGC------TG----------TTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCG------TCAGTGTTCATTTTCCCATCGAGTCAAGAGCACACACGGTCA----------GGAGCGCG----------
droKik1	scf7180000302706:2172587-2172707 +		G--CGGCGC------TG------CA----------GTCGA---CG---------TC-+-----GC---TGCCCTCGCC----------TCTGC---CGCCGAC-----TGA------TG----------TTGGGCGAATGCC--+----+---------TTTTTAG--------CGAGCTTCATCGTCAGTGTTCATTTCCCCATCGAATCGGCAACA-A--CGAGCG----------G------+----------
droFic1	scf7180000454104:908469-908579 -		CGACGTCG-------+------+----------+-----+---+----------+-----+---+---CTGCG----------GCTGCAATCGCCGACGCTCGTTTC------TGT----------GTTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droEle1	scf7180000491023:503305-503448 -		TGACTCTGC------TG------CT----------GCTGT--TGTTGCTGTGCTG-ATGTTG---A---TGCTGC----------+-----TGCTGATGCA----AGTGCATC-TGAGGCGGTGGCTGCGG----------TGC--CTGCTGCAGTTGC-+---------+---+---+---------+--GCG-----GTGGA----GGTGCGTTGTAGAACTGGCCAGCGG-GCGGCG----------GAGCAGGT----------
droRho1	scf7180000779228:19070-19178 +		CGACGTCG-------+------+----------+-----+---+----------+-----+---+---CTGCG----------GCTGCAGTCGCCGACGTCGCTTTC------TG----------TTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTTCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droBia1	scf7180000302402:3416414-3416549 +		G----CTGGCGTCGCCG------C----------GCCGT--CG---------GTG-GC---GC---TGCCGCCGCC----------ACTGCACTCGCCGACGTCGCTTTC------TG----------TTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCCACA-A--CGAGCG----------GAAGTCG-+----------
droTak1	scf7180000415245:186272-186388 -		CGCCGTGCA------CG------TC----------G----+----------+-----+---+---CCGTG----------GCTGCACTTGGCGACGTCGCTTTT------TCA----------GTTGGGCAATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droEug1	scf7180000409470:253101-253233 +		AAACGCAGC------TG------CA----------GTCGA---CG---------TC-+-----GC---TGCCA----------GCTGCTCGCTGCAATCGCCGACATTCGTTTC------TGTT----------+----TGGGCAATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAACCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
dm3	chr3R:5919844-5919974 +		TGACGTCGA------CG------CA----------GTGTT---AG---------GT-+-----GC---TGCCATCGCT----------GCTGCAGTCGCCGACGTCGCTTTC------TGTT----------+----TGGGCCATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droSim2	3r:15128586-15128716 -		CGACGTCGA------CG------CA----------GTGTT---CG---------GT-+-----GC---TGCCAGCGCT----------GCTGCACTCGCCGACGTCGCTTTC------TGTT----------+----TGGGCCATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droSec2	scaffold_0:15993565-15993695 -		CGACGTCGA------CG------CA----------GTGTT---CG---------GT-+-----GC---TGCCAGCGCT----------GCTGCACTCGCCGACGTCGATTTC------TGTT----------+----TGGGCCATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCG-+----------
droYak3	3R:9967383-9967541 +		CGACGTCGA------CG------CT----------ACTGC---TGCTGCTGCTGCCG-TTGCTGC---TGCCAGCGCT----------GCTGCATTCGCCGACGTCGCTTTC------TGTT----------+----TGGGCCATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCGCAGGGGGCCCACAG
droEre2	scaffold_4770:15680270-15680417 -		CGACGTCGA------CG------CA----------GGTTT---CG---------GT-+-----GCTGGCTGCGAGCGCT----------GCTGCATTCGCCGACGTCGCTTTC------TGTT----------+----TGGGCCATTGCC--+----+---------GT--TGG--------CGAGCT-----TCAGTGTTCATTTCCCCATCGAGTCGGCAACA-A--CGAGCG----------GAAGTCGCAGGGGGCCCACAG

Generated: 09/08/2015 at 08:19 PM

	PASS/FAIL
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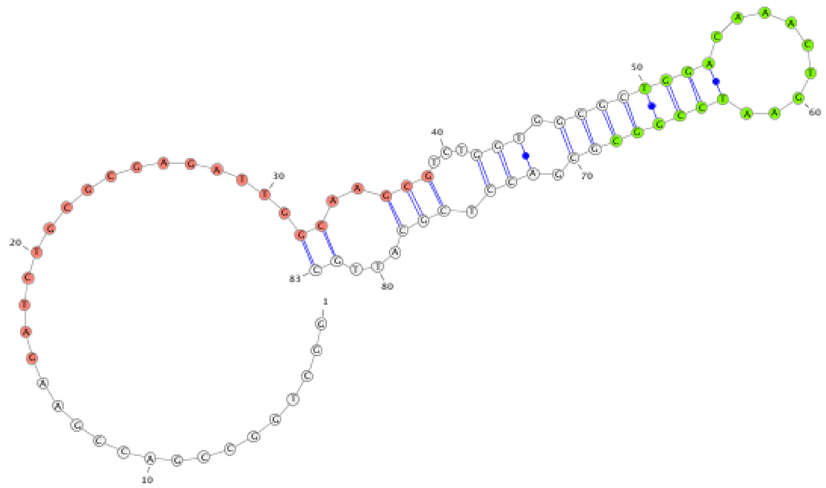
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	5
rescue.candidate	1

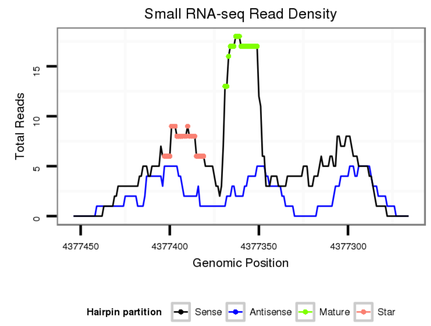
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3829	**XR_group6:4377316-4377404 -**	**candidate-rescued**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

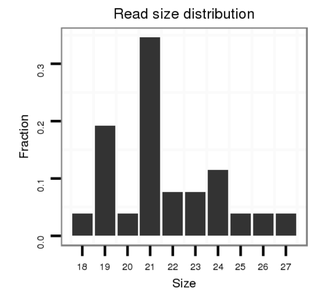
Legend: mature star mismatch in alignment mismatch in read

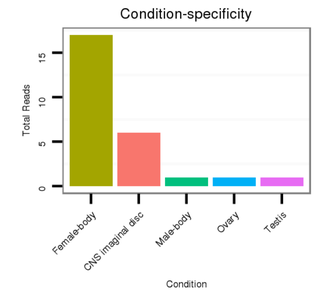
Predicted structure

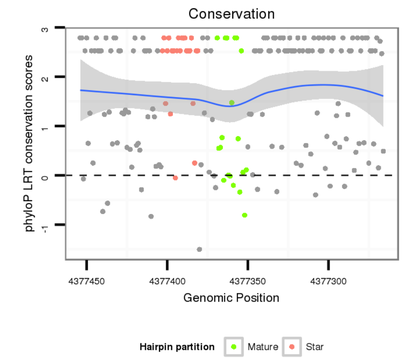


dps_3829_annot [-23.5]









Show Alternate Folds

Flybase annnotation

CDS [Dpse\GA23538-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATGAGGCGGAGGCGCATGCCTTTGCTACGGCCCAGGGCTGGCCGACCGAAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCGGGACTCGGTTGAAGAGTTTCCGGTCACA	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902012 CNS imaginal disc	V112 male body	M059 embryo	SRR902010 ovaries	SRR902011 testis	GSM444067 head
**********												
.....TGGACAAACTGAATCCGGC.....	19	0	1	3.00	3	1	2	0	0	0	0	0
.....GCTGGACAAACTGAATCCGGC.....	21	0	1	2.00	2	2	0	0	0	0	0	0
.....CTGGACAAACTGAATCCGGCGC.....	22	0	1	2.00	2	0	2	0	0	0	0	0
.....GACAAACTGAATCCGGCGCGA.....	21	0	1	2.00	2	2	0	0	0	0	0	0
.....TGGACAAACTGAATCCGGCGC.....	21	0	1	2.00	2	2	0	0	0	0	0	0
.....TGCTCATCCAGCGGGACTCGG.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....ATCCAGCGGGACTCGGTTGAAGA.....	23	0	1	1.00	1	1	0	0	0	0	0	0
.....TGCTCATCCAGCGGGACTCGGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....CTGGACAAACTGAATCCGGC.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....AGCGTCTGGTGGCGCTGGACAAAC.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....GACCTCGCATTGCCATACTAACGCAG.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....GATCCCGTGCTGCTCATCC.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....GATCTGCGCGAGATTGGCAAGCG.....	23	0	1	1.00	1	0	0	1	0	0	0	0
.....TGCGCGAGATTGGCAAGCGTCTGGTGG.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....CAGGGCTGTGATCCCGTGCTG.....	21	0	1	1.00	1	0	0	1	0	0	0	0
.....CGCATTGCCATACTAACGCAG.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....AAGATCTGCGCGAGATTGGCA.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TGTGATCCCGTGCTGCTCATC.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....GTGCTGCTCATCCAGCGGGACT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....AACGCAGGGCTGTGATCCCGT.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....GCTGGCCGACCGAAGATCTGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....AACTGAATCCGGCGCGACCTCGCA.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....TGCGCGAGATTGGCAAGCGTCTGG.....	24	0	1	1.00	1	1	0	0	0	0	0	0
.....CTGGACAAACTGAATCCGGCG.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TGCGCGAGATTGGCAAGCGTCTGGT.....	25	0	1	1.00	1	0	0	0	0	1	0	0
.....AAGATCTGCGCGAGATTGGC.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....TGCTCATCCAGCGGGACTCG.....	20	0	1	1.00	1	1	0	0	0	0	0	0
.....GACCGAAGATCTGCGCGAGATTGGC.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....CTACGGCCCAGGGCTGGCCGACCGAA.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....TTGGCAAGCGTCTGGTGGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....TGGACAAACTGAATCCGGCGCGA.....	23	0	1	1.00	1	0	0	0	0	1	0	0
.....GACAAACTGAATCCGGCGC.....	19	0	1	1.00	1	0	1	0	0	0	0	0
.....TGCCTTTGCTACGGCCCAGGGCTGG.....	25	0	1	1.00	1	1	0	0	0	0	0	0
.....ACAAACTGAATCCGGCGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0
.....ATACTAACGCAGGGCTGTGA.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....TGCTACGGCCCAGGGCTGGCCGACCGA.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....GCGACCTCGCATTGCCATACT.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....TGGCCGACCGAAGATCTGCGCGAGAT.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....ATCCCGTGCTGCTCATCCAGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

TTACTCCGCCTCCGCGTACGGAAACGATGCCGGGTCCCGACCGGCTGGCTTCTAGACGCGCTCTAACCGTTCGCAGACCACCGCGACCTGTTTGACTTAGGCCGCGCTGGAGCGTAACGGTATGATTGCGTCCCGACACTAGGGCACGACGAGTAGGTCGCCCTGAGCCAACTTCTCAAAGGCCAGTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M022 male body	SRR902010 ovaries	SRR902011 testis
**********									
.....CTAGACGCGCTCTAACCGTT.....	20	0	1	2.00	2	2	0	0	0
.....AGGCCGCGCTGGAGCGTAACG.....	21	0	1	1.00	1	1	0	0	0
.....ACTAGGGCACGACGAGTAGGT.....	21	0	1	1.00	1	1	0	0	0
.....CGACGAGTAGGTCGCCCTGAG.....	21	0	1	1.00	1	1	0	0	0
.....GCGTACGGAAACGATGCCGGGTC.....	23	0	1	1.00	1	0	0	0	1
.....CCCTGAGCCAACTTCTCAAAG.....	21	0	1	1.00	1	1	0	0	0
.....GAGTAGGTCGCCCTGAGCCAA.....	21	0	1	1.00	1	1	0	0	0
.....GTTTGACTTAGGCCGCGCTGG.....	21	0	1	1.00	1	1	0	0	0
.....CGGCTGGCTTCTAGACGC.....	18	0	1	1.00	1	0	1	0	0
.....TCGCAGACCACCGCGACCTGT.....	21	0	1	1.00	1	1	0	0	0
.....TTAGGCCGCGCTGGAGCGTAA.....	21	0	1	1.00	1	1	0	0	0
.....CCGGCTGGCTTCTAGACGCGC.....	21	0	1	1.00	1	1	0	0	0
.....GCGCTGGAGCGTAACGGTATG.....	21	0	1	1.00	1	1	0	0	0
.....CCTGTTTGACTTAGGCCGCGCT.....	22	0	1	1.00	1	1	0	0	0
.....GACGAGTAGGTCGCCCTGAGC.....	21	0	1	1.00	1	1	0	0	0
.....CGGCTGGCTTCTAGACGCGCT.....	21	0	1	1.00	1	1	0	0	0
.....GGTCGCCCTGAGCCAACTTCT.....	21	0	1	1.00	1	1	0	0	0
.....CCGGGTCCCGACCGGCTGGCT.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XR_group6:4377266-4377454 -	dps_3829	AATGAGGCGGAGGCGCATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCGGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droPer2	scaffold_9:2666447-2666635 -	dpe_2483	AATGAGGCGGAGGCGCATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCGGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droWil2	scf2_1100000004511:5276750-5276938 +	dwi_5417	AATGAGGCGGAGGCGCATGCCTTTGCCACGGCCCAGGGCTGGCCCACG---AAGATCTGCGCGAGATTGGCAAGCGACAGTACGTCGTCTGGACAAACTAATCCAAGTCGCGCCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTCGTCTGCTCATTCGAAAAGA---TTCGGTTGAAGAGTTTCCGGTCACA
droVir3	scaffold_13049:22492152-22492343 +	dvi_158	AACGAGGCGGAGGCGCAGCCTTTGCCACGGCCAAGGCTGGCCCGCCGCCACAATGATCTGCGTGAGATTGGCAAGCGCTCGTCGCGCTGAATAACCCAATACGGCGGCACCGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTTATACAGCACGA---TTCGGTCCACGAGTTTCCAGTCACA
droMoj3	scaffold_6680:1709712-17099903 +	dmo_114	AACGAGCCAGAGGCCATGCCTTTGCCACGGCCAAGGCTGGCCCGCCGCCATCGATGTCGCGTGAGATTGGCAAGCGTCTGGTTGGCACTGCCCAAATCCAATTCACAGCGACCGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTCATCCAGCACGA---CAACGGTCCACGAGTTTCCCGGTCACA
droGri2	scaffold_15121:203613-203807 +	dgr_465	AATGAGGCGGAGGCGCAGCCTTTGCCACGGCCAAGGCTGGCCCCCCATCGATCTGCGTGAGATTGGCACGCGCTCTGGTTGGCACTGAAGAACTGAATTCACGGCGGCACCGCATTGCCATACTCACGCAGGGCTGTGATCCCGTGCTGCTCTGTCCAGCAGGAGGCTCGGTTCCACGAGTTTCCAGTCACA
droAna3	scaffold_13337:4137395-4137583 +	dan_4038	AACGAGGCGGAGGCGCAGCCTTTGCCAGGCCAGGCTGGCCGATGT---GGGATCTGCGAGAGATTGGCAAGCGCTGGTGGCGTCGAAACCTGAATCCGCAGCGACCGCATTGCCATACTCACGCAGGGCTGTGATCCCGTGCTGCTCTTCCAGCAGGA---CTCGGTCCACGAGTTCCGGTCACA
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droEle1	scf7180000491255:1412089-1412277 -		AACGAGGCGGAGGCACAGCCTTCGCCAGGCCCAGATGGCCGACG---GGGATCTGCGCGAGATTGGCAAGCGCTGGTGGCGTGGACAAGCCTGAATCCGACGCGACCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTGCTGCTCATCCAGCAGGA---TTCGGTCCACGAGTTCCGGTCAGG
droRho1	scf7180000769477:967-1151 +		AACGAGGCGGAGGCACAGCCTTCGCCAGGCCCAGATGGCCGACG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGCTGGACAAACTGAATCCGGCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTGCTGCTCATCCAGCAGGA---TTCGGTCCACGAGTTCCGGT----
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droTak1	scf7180000415706:66147-66335 -		AACGAATCGGAGGCTCAGCCTTCGCCAGGCCCAGATGGCCGACG---GGGATCTGCGCGAGATTGGCAAGCGCTGGTGGCGCTGGACAACCTGAATCCGGCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTCTGCTCATCCAGCAGGA---CTCGGTCCACGAGTTCCGGTCACG
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droSim2	3L:13294025-13294213 -	dsi_3245	AACGAGGCGGAGGCGCAGCCTTCGCCAGGCCCAGCAGTGGCCGACG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGTGGACAAGAAAACCCCGACGCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCTGTCTGCTCATCAAGCAGGA---TTCGGTCCACGAATTCCCGGTCACG
droSec2	scaffold_015185161-5185349 -	dse_1846	AACGAGGCGGAGGCGCAGCCTTCGCCAGGCCCAGCAGTGGCCGACG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGTGGACAAGAAAACCCCGGCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCTGTCTGCTCATCAAGCAGGA---TTCGGTCCACGAGTTCCGGTCACG
droYak3	3L:13092479-13092667 -	dya_1798	AACGAGGCCAGAGGCTCAGCCTTCGCCAGGCCCAGCAGTGGCCGACG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGTGGACAAGAAAACCCCGACGCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCTGTGCTGCTCATCAAGCAGGA---TTCGGTCCACGAGTTCCGGTCACG
droEre2	scaffold_4784:13021109-13021297 -	der_1523	AACGAGGCGGAGGCTCAGCCTTCGCCAGGCCCAGCAGTGGCCGACG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGTGGACAAGAAAACCCCGAGCGACCGCATTGCCATACTCACGCAGGGCTGCGATCCTGTGCTGCTCATCCAGCAGGA---TTCGGTCCACGAGTTCCGGTCACG

Generated: 09/08/2015 at 08:19 PM

	PASS/FAIL
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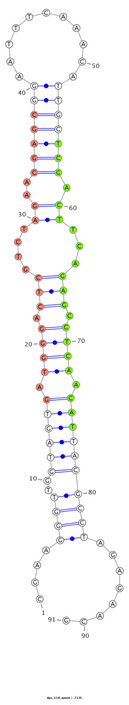
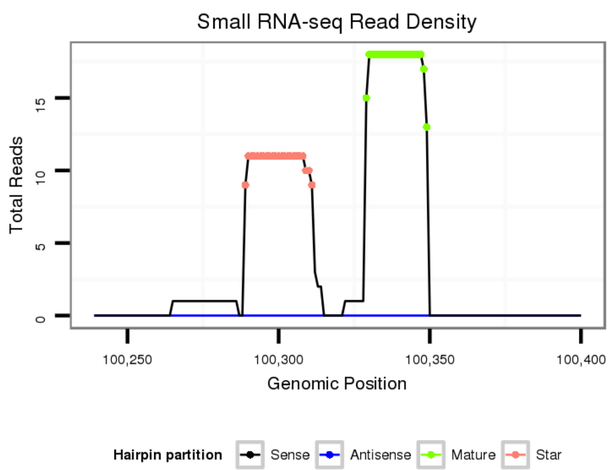
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	0
crit.ptop3	0
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

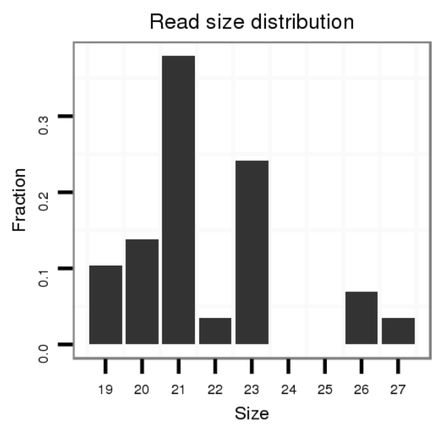
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_110	**XL_group3b:100289-100350 +**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

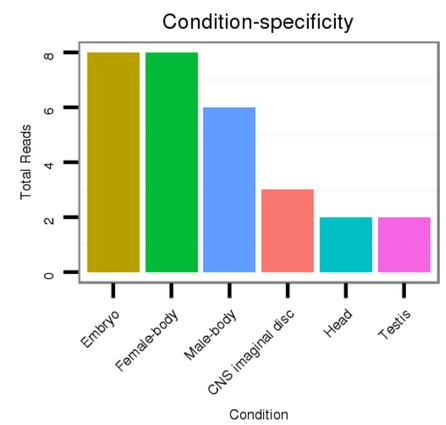
Legend: mature star mismatch in alignment mismatch in read

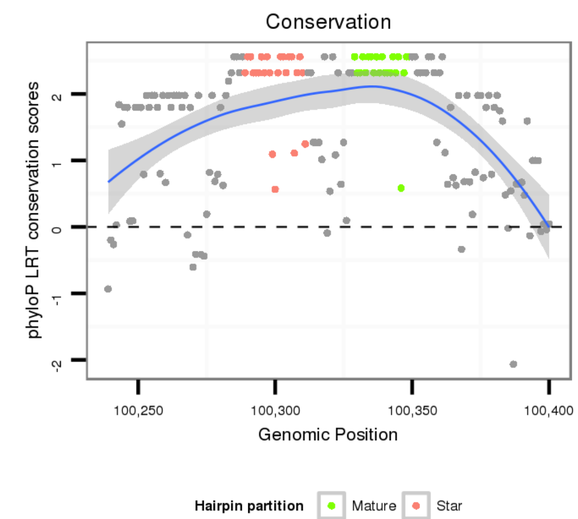
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA10815-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACAAAAGCGTGGGTACTTGTTTTGAAAGAACATATCGAAGGGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTCAAACATTGCTCGACTTCAGAGCCTCAACATTACGCCTAGAGAACGCAAGCAGCTTTCGACCATGCATCCCACCAGCGAACG **********....((((..((((((.((((.(((....((..(((((((.....)))))))..))...)))).))))).))))))))))..).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V112 male body	M040 female body	M059 embryo	GSM343916 embryo	SRR902012 CNS imaginal disc	GSM444067 head	SRR902011 testis	M062 head	M022 male body
.....TCGACTTCAGAGCCTCAACAT.....	21	0	1	11.00	11	4	3	3	0	0	1	0	0	0
.....GATGGGACTCGTCTAGAACGAGC.....	23	0	1	6.00	6	0	0	1	0	3	0	1	1	0
.....CGACTTCAGAGCCTCAACAT.....	20	0	1	2.00	2	0	0	0	2	0	0	0	0	0
.....TCGACTTCAGAGCCTCAACA.....	20	0	1	2.00	2	0	2	0	0	0	0	0	0	0
.....GATGGGACTCGTCTAGAACGAGCGGA.....	26	0	1	2.00	2	1	0	0	1	0	0	0	0	0
.....GATGGGACTCGTCTAGAACGAG.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....AGAACATATCGAAGGGTTGGTA.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....CGACTTCAGAGCCTCAACA.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ATGGGACTCGTCTAGAACG.....	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0
.....ATGGGACTCGTCTAGAACGAGCG.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....ACATTGCTCGACTTCAGAGCCTCAACA.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....TCGACTTCAGAGCCTCAAC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

TGTTTTCGCACCCATGAACAAAACTTTCTTGTATAGCTTCCCAACCATCACTACCCTGAGCAGATCTTGCTCGCCTTAAAGTTTGTAACGAGCTGAAGTCTCGGAGTTGTAATGCGGATCTCTTGCGTTCGTCGAAAGCTGGTACGTAGGGTGGTCGCTTGC **********....((((..((((((.((((.(((....((..(((((((.....)))))))..))...)))).))))).))))))))))..).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V112 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	XL_group3b:100239-100400 +	dps_110	ACA---AAAGCGTGGGTACTTGTTTTGAAAGAACATA----TC--GAAG---GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCA-AGCAGCT--TTCGACCA-TGCATCCCACC-AGC----GAACG---
droPer2	scaffold_56:124045-124205 +	dpe_157	ACA---AAAGCGTGGGTACTTGTT-TGAAAGAACATA----TC--GAAG---GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCA-AGCAGCT--TTCGACCA-TGCATACCACC-AGC----GAACG---
droWil2	scf2_1100000004515:1719065-1719069 -		GCA---AA----------GGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCA-AGCAGCT--TTCGACCA-TGCATACCACC-AGC----GAACG---
droVir3	scaffold_12970:5369119-5369199 -	dvi_24642	---GGTAGTGATGGGACTCACCTAGAACGAGTGGAATATT--AAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA-GAC-AACAGCT--TTAGATCAATGGCA----ACCCGCTTA-GGAAG---
droMoj3	scaffold_6473:4951753-4951833 -	dmo_3154	---GGTAGTGATGGGACTCACCTAGAACGAGTGGAATATTT--TAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA-GAC-AACAGCT--TTAGATCAATGGCA----ACCCGCTTA-GGAAG---
droGri2	scaffold_15203:9467769-9467849 +		---GGTAGTGATGGGACTCAACTAGAACGAGTGGAATTTTAAAAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGA--GAC-AACAGCT--TTAGATCAATGGCA----ACCCGCTTA-GGAAG---
droAna3	scaffold_13334:472140-472306 +	dan_4039	ATG---GAAGC--GGGAACTTGTTCTGAAAGATCAAA--CAAT-TTAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTT-GAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCTTAGAGAAAAGAC-AACAGCT--TTAGATCAATGGCA----ACCCGCTTA-GGAAG---
droBip1	scf7180000396431:1081228-1081392 -		---GGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTC-AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGACCAGAC-AACAGCTTTTTAGATCAATGA---CCACCC-GCTTGGCGAAGTAC
droKik1	scf7180000302698:307823-307977 -		ACA---TAAGC--GGGAACTTGTTCTGAAAGACCAATACAAA-ATAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAATT--TTAGATCAATGGGA----CCC----
droFic1	scf7180000454073:1443011-1443156 +		---GGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAACCGAC-AACAGCT--TTAGATCAATGGGA----CCC----
droEle1	scf7180000491044:215079-215229 +		ATA---TAAGC--GGGAACTTGTTCTGAAAGACCCTA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGCGAAC-GACAACTAGCT--TTAGATCAATGGGA----CCC----
droRho1	scf7180000779510:38402-38543 +		CTC---TAAGC--GGGAACTTGTTCTGAAAGACCTA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGCATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCAA----------
droBia1	scf7180000302041:563684-563832 +		CTC---TAAGC--GGGAACTTGTTCTGAAAGACCCA----GA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AGCCGCGCTCG-ACTTCAGAGCCTCAGCATTACGCC-TAGAGAAC-GAC-ATCAGCT--TTAGATCAATGGGA----CCC----
droTak1	scf7180000414393:30853-30988 -		---GGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCGTCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCAA----------
droEug1	scf7180000408958:35942-36101 -		---GGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCAATGGGA----CCCCGCTTAGGAGAA---
dm3	chrX:13553569-13553711 +	dme_424	CCA---TAAGC--GGGAACTTGTCTGAAAGACCCA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAATGAGTGGAAATTCA-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGCT--TTAGATCAT----------
droSim2	x:12890288-12890429 +	dsi_32459	CCA---TAAGC--GGGAACTTGTCTGAAAGACCCA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGCT--TTAGATCAT----------
droSec2	scaffold_20:193510-193651 +	dse_1847	CCA---TAAGC--GGGAACTTGTCTGAAAGACCCA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGCT--TTAGATCAT----------
droYak3	X:7836410-7836562 +	dya_1799	ACAATGTAAGC--GGGAACTTGTTCTGAAAGACCCA----AA--TAAG---AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCAATGGGA----CCC----
droEre2	scaffold_4690:13329677-13329820 -	der_1524	---GGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCAATGGGA----CCC----

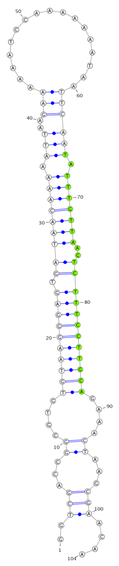
Generated: 09/08/2015 at 08:19 PM

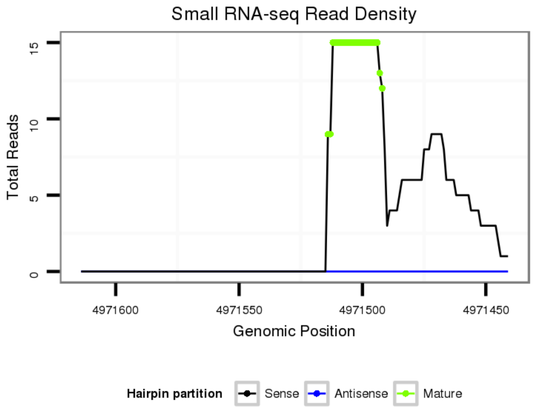
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

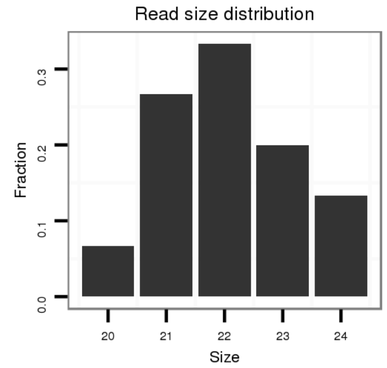
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3834	**4_group1:4971491-4971564 -**	**candidate-rescued**	**Mirtron**	**5pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

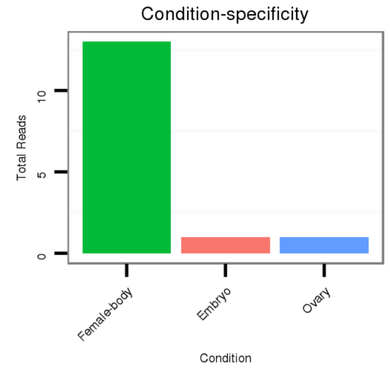
Legend: mature star **mismatch in alignment** mismatch in read

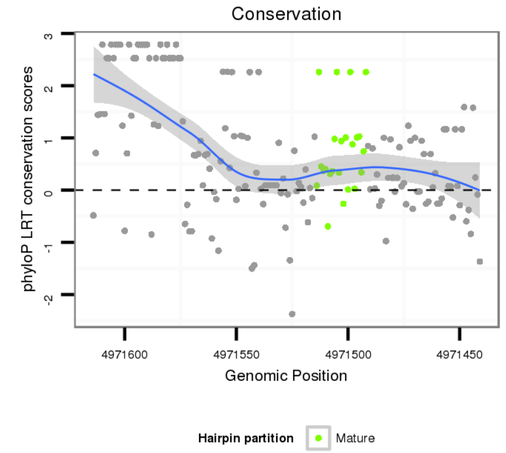
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_2731]; utr5 [utr5_plus_2732]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
TTTAATCCAGTTTCGATTGGTTATTGTGGAAGGTCGGTCGACCGGCGTGTGTAAGGGAGTGATAACAAAAATTAAGAAAAAATCCAAAAAAATAATTCAATATTTGTTAACTCTTTCCTTGCAGAAACTAAGCGAACAAGAAGGAGGCTTTAAGGAGTAACCAAGAACCTATGC
**********************************..(((...((....((((((((((.(((((((((.(((..(((.................))))))).)))))))..)))))))))))....))...)))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902010 ovaries	GSM343916 embryo	GSM444067 head	V112 male body	
23	0	1	3.00	3	3	0	0	0	0	TATTTGTTAACTCTTTCCTTGCA
23	1	1	3.00	3	2	1	0	0	0	TTTGTTAACTCTTTCCTTGCAGT
22	0	1	3.00	3	2	0	1	0	0	TTTGTTAACTCTTTCCTTGCAG
24	0	1	2.00	2	1	1	0	0	0	TATTTGTTAACTCTTTCCTTGCAG
22	0	1	2.00	2	2	0	0	0	0	TATTTGTTAACTCTTTCCTTGC
25	0	1	2.00	2	2	0	0	0	0	AGAAACTAAGCGAACAAGAAGGAGG
21	0	1	2.00	2	2	0	0	0	0	TTTGTTAACTCTTTCCTTGCA
21	0	1	2.00	2	2	0	0	0	0	TATTTGTTAACTCTTTCCTTG
23	0	1	1.00	1	1	0	0	0	0	CTTTAAGGAGTAACCAAGAACCT
22	0	1	1.00	1	0	0	0	1	0	AGCGAACAAGAAGGAGGCTTTA
23	0	1	1.00	1	0	0	0	0	1	AACTAAGCGAACAAGAAGGAGGC
20	0	1	1.00	1	1	0	0	0	0	TTTGTTAACTCTTTCCTTGC
27	0	1	1.00	1	1	0	0	0	0	GGAGGCTTTAAGGAGTAACCAAGAACC
24	0	1	1.00	1	1	0	0	0	0	GAAACTAAGCGAACAAGAAGGAGG
23	0	1	1.00	1	1	0	0	0	0	GAAGGAGGCTTTAAGGAGTAACC
19	0	1	1.00	1	0	0	1	0	0	GAAGGAGGCTTTAAGGAGT
19	0	1	1.00	1	1	0	0	0	0	AAGCGAACAAGAAGGAGGC
21	2	1	1.00	1	1	0	0	0	0	TATTTGTTAACTCTTTCCTGC
27	0	1	1.00	1	1	0	0	0	0	CTTTAAGGAGTAACCAAGAACCTATGC

Anti-sense strand reads

```
AAATTAGGTCAAAGCTAACCAATAACACCTTCCAGCCAGCTGGCCGCACACATTCCCTCACTATTGTTTTTAATTCTTTTTTAGGTTTTTTTATTAAGTTATAAACAATTGAGAAAGGAACGTCTTTGATTCGCTTGTTCTTCCTCCGAAATTCCTCATTGGTTCTTGGATACG
**********************************..(((...((....((((((((((.(((((((((.(((..(((.................))))))).)))))))..)))))))))))....))...)))....**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	4_group1:4971441-4971614 -	dps_3834	TTTAATCCAGTTTCGATTGGTTATTGTGGAAGGTCGGTCGACCGGC----GTGTGTAA---GGGAGTGATAACAAA---AA-TTAAGAAAAAATCCAAAA---AAATAAT-------T--------------CAATA------TTTGTTAA-----------CTCTTTCCTTG---CAGAAACTAA---GC--G----------------AACAA----------------------------GAAGGAGG-----CTTTAAGGAGTAACCAAGAAC-CTAT--G-C-
droPer2	scaffold_5:245797-245970 +	dpe_116	TTCAATCCAGTTTCGATTGGTTATTGTGGAAGGTCGGTCGACCGGC----GTGTGTAA---GGGAGTGATAACAAA---AA-TTAAGAAAAAATCCAAAA---AAATAAT-------T--------------CAATA------TTTGTTAA-----------CTCTTTCCTTG---CAGAAACTAA---GC--G----------------AACAA----------------------------GAAGGAGG-----CTTTAAGGAGTAACCAAGAAC-CTAT--G-C-
droWil2	scf2_1100000004585:4878966-4879177 -	dwi_5418	ATTTAACCAGTTTCAATTGGTTATTGTGCAGGTCGGTCGATTAA-CACAGTG-GTAT---GGAAGAGATAGCAAA---AAGTTCAA-------------------TTAAAAATGTACAATCTTGACTAAATCAACA------TTTGTTAA-----------CTCTTCCTA---CAGACAC-AA---CT--GAACATA---------ACCGCAGAAATAGCAACAACTACAACAACTACAAA-GAGGAGGAGATAACTACAAGGC-----------AAAT--G-T-
droVir3	scaffold_13246:2198397-2198436 -		TATTAACCAGTTTCGTTGGTTATTGCGGCAGGTCGGTCG--
droMoj3	scaffold_6500:26320838-26320883 -		ATTTAACCAGTTTAAGTTGGTTATTGCGGCAGGTCGGTCGATAGG--
droGri2	scaffold_15126:3759888-3759938 +		TCTTAACCAGTTTCGTTGGTTATTGTGGCAGGTCGGTCGTTGAA--
droAna3	scaffold_12943:3625657-3625804 -	dan_4041	TTTTAACCAGTTTCAATCGGTTATTGCGGCAGGTCGGTCGAGT---------------AA---GGGAGTGATAACAAA---AA-TTCAGT-------CAA-GT---CCATTAA-------C--------------CAATA------TTTGTTAA-----------CTCTTTCCTTGCAG-ATATTACTAA---AC--G--CA-------------CAAA----------------------------G-A-----------------CAAGTAACCAAAAAA-AAAA--G-A-
droBip1	scf7180000396433:509897-510043 -		ATTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGAGT---------------AA---GGGAGTGATAACAAA---AA-TTAAGT-------CAAGAC---CAA-TAA-------C--------------CAATA------TTTGTTAA-----------CTCTTTCCTTG---CAGATACCAAA---C--G--GATACTAACCCAAAAAAACAAAA----------------------A-----------------AG---AA-TT-
droKik1	scf7180000302643:149849-150009 +		TTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGAGT----------G---AGAGGCCTGTGTTAAAAAA---AA-TCAAGT-------CAAAAATCGAAAATAA-------A--------------CATTA------TTTATAA-----------CTCTTTCCTTGCAG-AGATACCCAA-----CCA-------------------A----------------------AGAGCAAA-----C----CGGAATAGAAAGGAAG-AGAA--A-C-
droFic1	scf7180000453842:593650-593794 +		TTTTAACCAGTTTCGATTGGTTATTGTGGCAGGTCGGTCGACCCC----------CA---GAGAGTGATGATAAA---AA-TAAAGT-------CAAAAA---GAGTTTA-------C--------------TTATA------T-GA--TACTACTTT--TTCCTCTCTCCTTG---CAGTTAACAA-----A-----ACAGA---------GCTAGTAAA----------------------A-----------------A-G----CT-
droEle1	scf7180000491186:1152340-1152472 +		CTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGATT-----------TT---GGCAGTGATAATAAA--AAA-GGAAGG-------CAAGCC---AAATATA-------C--------------TAATA------TTTATTTA-----------CCATCTGATTG---CAGTTAACTAA-----A-----TCACA---------GGAATTAAC----------------------G-----------------A----A-A-
droRho1	scf7180000771933:31915-32052 +		TTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGATT-----------TT---GGAAGTGATAGTAAA---AA--AAAGG-------CAAGCC---GAATGTA-------C--------------TGATAATATATTCTCCTTA-----------TTTTCTCCTTG---CAGTTAACCAA-----A-----ACACA---------GTAACTAAG----------------------A-----------------A--A----A-A-
droBia1	scf7180000302422:6989066-6989202 -		TTTTAACCAGTTTCGATTGGTTATTGTTCAGGTCGGTCGAGT---------TG---AAGAGTGCTAATAAC---AA-CAAAAG-------TAAAC---GAATTAA-------C--------------TTATA------TTTGTTTACT---------CTCTCTCCTTG---CAGTTAAAAAAG---A-GGGCA---------GGAACTAAG----------------------A-----------------A--A----A-A-
droTak1	scf7180000415708:336730-336871 -		ATTTAACCAGTTTCGATTGGTTATTGCGGCAGGTCGGTCGAGT---------TG---AACAGTGATATTAAA---AA-GAAGG-------TCGAT---GATTTCA-------C--------------TAACA------CTTATTTA-----------C--TTTGATTG---CAGTTAACAAAAACGAA-GCACA---------TCAACTTAA----------------------A-----------------A-GG-AA--A-C-
droEug1	scf7180000409767:196156-196315 -		TTTTAACCAGTTTCGATTGGTTATTGCGGCAGGTCGGTCGATC---------TCATTCCCAGTGATAATAAA---CA-AAAAAT-------TCAGTTACCAG-TTG-------C--------------TAATA------TCTATTTCCT---------CTCTCTCCTTG---CAGTTAACACA-----A-----AAACA---------AGAACTAAC----------------------A-----------AACCATAACTAAAAAG-GTAA--A-C-
dm3	chr2L:21114468-21114624 +		TTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGAGT---------TG---AAGAGTGATACTAAT---AA-AAAAGG-------CAAGAT---GAACTTAAACATGAA--------------CAAAA------TTGACTTCTCTTTTTCTC--TTTTCTCCTGG---CAGGTGAAGAA-----A-----ACATA---------GCAGCTGAA----------------------A-----------GG---AACCTG
droSim2	2L:20546304-20546453 +		CTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGAGT---------TG---AAGAGTGATACTACA---AA-TAAAGG-------CAAGAT---TAACTTA-------A--------------CAAAA------TTGACTTCTCTTTTTTTCTCTTTGG---CAGGTGAAGAA-----A-----ACATA---------GCAGCTGAA----------------------A-----------GG---AACCT-
droSec2	scaffold_18:1032819-1032968 +		TTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGAGT---------TG---AAGAGTGATACTACA---AA-TAAAGG-------CAAGAT---TAACTTA-------A--------------CAAAA------TTGACTTCTCTTTTTTTCTCTTTGG---CAGGTGAAGAA-----A-----ACATA---------GCAGCTGAA----------------------A-----------GG---AACCT-
droYak3	2R:1654704-1654851 -		TTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGAGT---------TG---AAGAGTGATACCAATAAAAA-GGAAGG-------CAAGAT---AAACTTA-------T--------------TAAAA------TTGA-TTCTCT-----T--TTTTCTCCTTG---CAGGTCAAGAA-----A-----ACATT---------AGAGCTGAAAA----------------------A-----------GG---AACCT-
droEre2	scaffold_4845:3378455-3378599 -		TTTTAACCAGTTTCAGTTGGTTATTGTGGCAGGTCGGTCGAGT---------TG---AAGAGTGATAGTGATAAGAA-TTAAGG-------CA-GAT---AAACTTA-------T--------------CGAAA------CTGGTGTACTCTT-------T--TATCCTTT---TAGGTAAGAA-----A-----ACATA---------ACAGCTGAAAA----------------------A-----------GG---AAC-C-

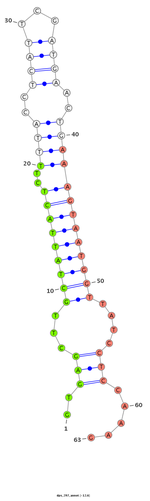
Generated: 09/08/2015 at 08:17 PM

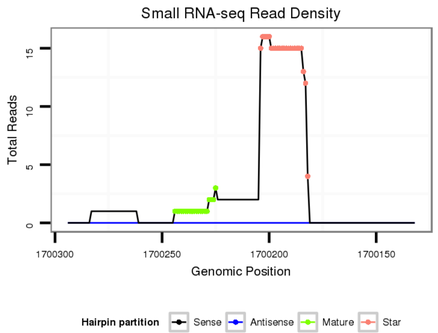
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	2

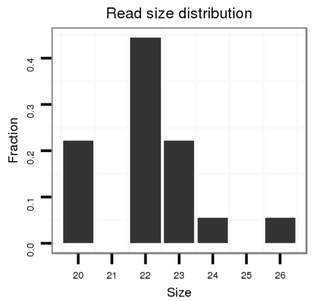
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_297	**2:1700182-1700244 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

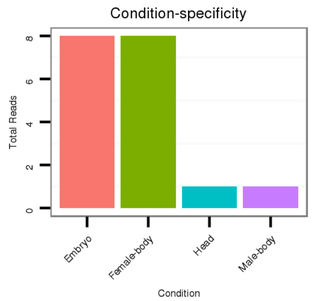
Legend: mature star **mismatch in alignment** mismatch in read

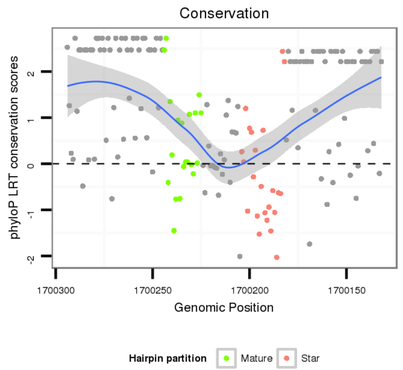
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dpse\GA10500-in]; CDS [Dpse\GA10500-cds]; CDS [Dpse\GA10500-cds]; utr3 [utr3_plus_6715]; utr3 [utr3_plus_6716]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCCTGCGCGGTGGCTACAGCACCGTGGAGAGTCTGAGCAATCGAGACAGGTGAGCTTGCTATTACTCTTTTACCTCATTCGATGAACTGAAAGTAATGGTTATCCTCCAAAGATGTCGAGTGGGCCAGATATCCCTATACGATGGCCCGCTGGCGCAGTTCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	GSM343916 embryo	M062 head	V112 male body
**********..(((...((((((((((..((((..((((...))))..))))))))))))))....))).....										
.....AAAGTAATGGTTATCCTCCAAA.....	22	0	1	8.00	8	2	3	2	0	1
.....AAAGTAATGGTTATCCTCAAAG.....	23	0	1	4.00	4	2	2	0	0	0
.....AAAGTAATGGTTATCCTCCA.....	20	0	1	2.00	2	1	0	0	1	0
.....TGGCTACAGCACCGTGGAGAGT.....	22	0	1	1.00	1	0	0	1	0	0
.....AAGTAATGGTTATCCTCCAA.....	20	0	1	1.00	1	1	0	0	0	0
.....GTGAGCTTGCTATTACTCTT.....	20	0	1	1.00	1	0	0	1	0	0
.....TTTACCTCATTCGATGAACTGAAAGT.....	26	0	1	1.00	1	1	0	0	0	0
.....TCTTTTACCTCATTCGATGAACTG.....	24	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CCGGACGCGCCACCGATGTCGTGGCACCTCTCAGACTCGTTAGCTCTGTCCACTCGAACGATAATGAGAAAATGGAGTAAGCTACTTGACTTTCATTACCAATAGGAGGTTTCTACAGCTCACCCGGTCTATAGGGATATGCTACCGGGCGACCGCGTCAAGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body
**********..(((...((((((((((..((((..((((...))))..))))))))))))))....))).....						

Show Alignment With Reads

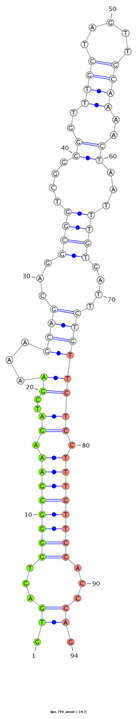
Re-alignment of all predicted orthologs

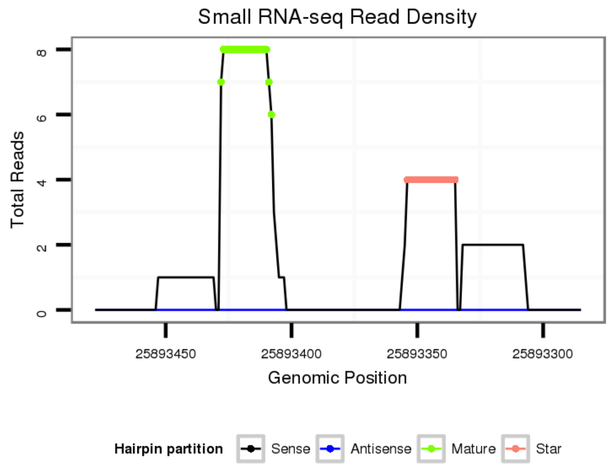
Species	Coordinate	ID	Alignment
dp5	2:1700132-1700294 -	dps_297	GGCCTGCGCGGTGGCTACAGCACCGTGGAGAGTCTGAGCAATCGAGACAGGTGAG----------CT----------TGC----------TATTACTCTTTTACCTCATTCG-A----T----GAAC----------T-GAAAGTAATGGTTA--T--CCTCCAAAGATGTCGAGTGGGCCAGATATCCCTATACGATGGCCCGCTGGCGCAGTTCG
droPer2	scaffold_7:1854046-1854208 -	dpe_2494	GGCCTGCGCGGTGGCTACAGCACCGTGGAGAGTCTGAGCAATCGAGACAGGTGAG----------CT----------TGC----------TATTACTCTTTTACCTCATTCG-A----T----GAAC----------T-GAAAGTAATGGTTA--T--ACTCCAAAGATGTCGAGTGGGCCAGATATCCCTATACGATGGCCCGCTGGCGCAGTTCG
droWil2	scf2_1100000004902:9560729-9560897 -		GGTTGCGAGGTGGTACAGTACCGTGAGAAGTCTGAGCAATCGGAGAGTCAG----------ACAAAA----------TATTAAGAAATCGCTTTACAAAAACCCTTAACGAA----------T----T----T----

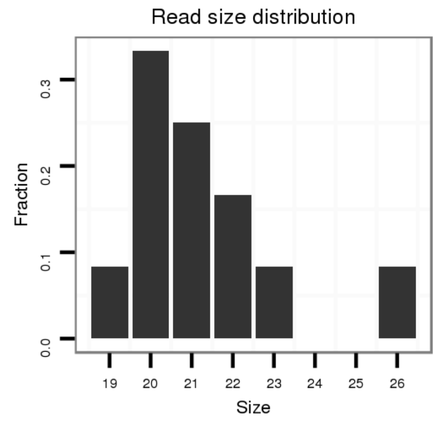
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_794	**2:25893335-25893428 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

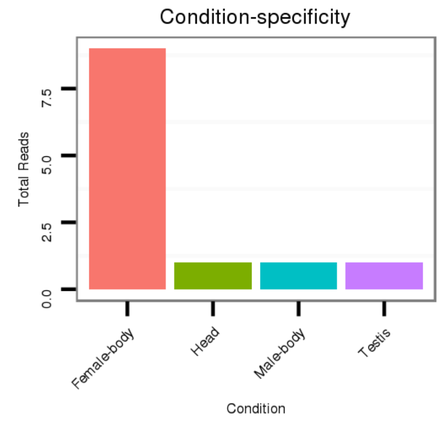
Legend: mature star mismatch in alignment mismatch in read

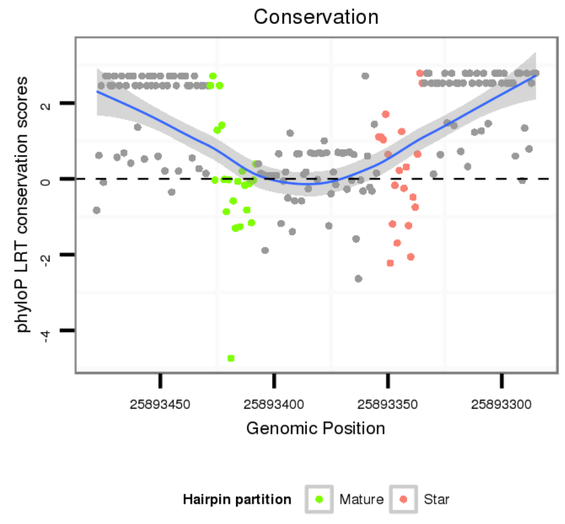
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA26236-in]; CDS [Dpse\GA26236-cds]; CDS [Dpse\GA26236-cds]; CDS [Dpse\GA26236-cds]; CDS [Dpse\GA26236-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCCCATGGATGAAGTCAGTCAACAGAGCACGCTCTCGAATGCATCAGCGGGTGAGTGGGGCGAAAGATCGAAAAGCAGCAGGCGGTCGGGGGTTTGCTAGTTGCAAAACTAATTTGTGATTCTGTTCTCCTTTGTTCCACCCAGCATCCGGCGAAGATCCCCAATGCACCACACCAAAGTCGCGCAAGAATGAT **********.((...((((((((.((..((...((((...((((....((..((((.....))))..))...))))....))))))))).)))))))...)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	V112 male body	GSM343916 embryo	SRR902011 testis	GSM444067 head
.....GTTCTCCTTTGTTCCACCCAGT.....	22	1	1	5.00	5	2	2	0	1	0	0
.....GTGAGTGGGGCGAAAGATCGA.....	21	0	1	2.00	2	1	0	1	0	0	0
.....TTCTCCTTTGTTCCACCCAGT.....	21	1	1	2.00	2	1	1	0	0	0	0
.....TTCTCCTTTGTTCCACCCAG.....	20	0	1	2.00	2	2	0	0	0	0	0
.....AGCACGCTCTCGAATGCATCAGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TGAGTGGGGCGAAAGATCGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGTTCTCCTTTGTTCCACCCAG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCCGGCGAAGATCCCCAATGCACCAC.....	26	0	1	1.00	1	0	0	1	0	0	0
.....GTGAGTGGGGCGAAAGATCGAAAAGC.....	26	0	1	1.00	1	0	0	0	0	1	0
.....GTGAGTGGGGCGAAAGATCGAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTCTCCTTTGTTCCACCCAGTT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TCCGGCGAAGATCCCCAATGCACCA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTTCTCCTTTGTTCCACCCAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGGGGCGAAAGATC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGTGGGGCGAAAGATCGAAAAGA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGGGGCGAAAGATCG.....	20	0	1	1.00	1	0	0	0	0	0	1
.....GTGAGTGGGGCGAAAGATCGAAA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCTCCTTTGTTCCACCCAGT.....	20	1	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CGGGTACCTACTTCAGTCAGTTGTCTCGTGCGAGAGCTTACGTAGTCGCCCACTCACCCCGCTTTCTAGCTTTTCGTCGTCCGCCAGCCCCCAAACGATCAACGTTTTGATTAAACACTAAGACAAGAGGAAACAAGGTGGGTCGTAGGCCGCTTCTAGGGGTTACGTGGTGTGGTTTCAGCGCGTTCTTACTA **********.((...((((((((.((..((...((((...((((....((..((((.....))))..))...))))....))))))))).)))))))...)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	SRR902011 testis

Show Alignment With Reads

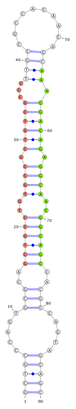
Re-alignment of all predicted orthologs

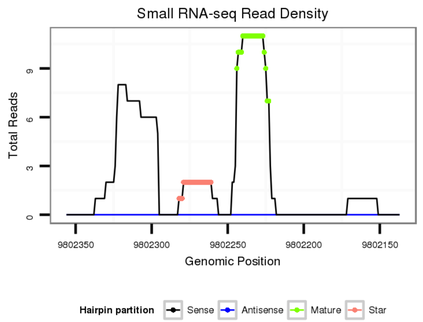
Species	Coordinate	ID	Alignment
dp5	2:25893285-25893478 -	dps_794	GCCCATGGATGAAGTCAGTCAACAGAGCACGCTCTCGAATGCATCAGCGGGTGAGTGGGGC--G-AAAGATCGAAAAGCAGCAGGCGG-TCGGGGGTTTGCTAGTTGCA----AAACTAATTTGT--GAT-------T-CTGTTCTCCTTT-G--TTCCA-----CCCAGCATCCGGCGAAGATCCCCAATGCACCACACCAAAGTCGCGCAAGAATGAT
droPer2	scaffold_6:1226872-1227065 -	dpe_2490	GCCCATGGATGAAGTCAGTCAACAGAGCACGCTCTCGAATGCATCAGCGGGTGAGTGGGGC--G-AAAGATCGAAAAGCAGCAGGCGG-TCGGGGGTTTGCTAGTTGCA----AAACTAATTTGT--GAT-------T-CTGTTCTCTTTT-G--TTCCA-----CCCAGCATCCGGCGAAGATCCCCAATGCACCACACCAAAGTCGCGCAAGAATGAT
droWil2	scf2_1100000004921:1526531-1526701 -		GCCCATGGATGAAGTTAGTCAACAGAGTACGCTCTCTAATGCATCCGCGGGTAAGTAGAAT--TGACG--CAGAA----------------------TTATGCCAGTTGAATGGCAAACTAATACTCT--CAC--ACG-TCT----------T--TGTTT-----TGCAGCATCCGGTGAAGATCCACAATGCACCACACCAAAGTCGCGCAAAAATGAT
droVir3	scaffold_12855:10044836-10044991 -		ACCAATGGATGAAGTTAGTCAACAGAGCACACTTTCAAATGCGTCAGGTGGTGCGTACCTT--TA-AA---TAAATGT----------TA----------AG----------ACGAAT--AACTGAGA-CT-TTG---------T--CATGT-----TACAGCATCAGGCGAAGATCGACAATGTACCACACCAAAGTCGCGCAAACATGAT
droMoj3	scaffold_6540:4000775-4000930 -		ACCAATGGATGAAGTCAGTCAACAGAGTACGCTCTCAAATGCGTCTGCAGTGCGTAATCT--G--AA--TGAGTTAT----------TT----------AT----------GTTCGT--AACTGAGG-CT-CT-----C----T--CGTCT-----TGCAGCATCCGGTGAAGATCCACAGTGTACCACCCAAAGTCGCGCAAACATGAT
droGri2	scaffold_14830:1233927-1234091 -		CCCAATGGATGACGTTAGTCAACAGAGCACGCTCTCGAATGCATCCGGTGGTGCGGTATAAT--TAACAATAT-----A-----GACATT-GCGGCGT----------GTGCTT--AACTGAGA-CT-CTGTTC------------TGTT-----TGCAGCATCGGGCGAAGATCCACAATGTACTACACCAAAGTCGCGCAAACATGAT
droAna3	scaffold_12911:2122398-2122559 +		CCCAATGGACGAAGTCAGCCAACAGAGCACGCTTTCGAATGCATCAGCGGGTAAGTGGATC--GTGTG--TGAAATAA------ATC--------------------A----------AGTAGG--TACTAATA-AC-GTATTC----CA---TTTGG-----CACAGCATCCGGCGAAGATCCTCAATGCACCACACCAAAGTCGCGCAAGAACGAT
droBip1	scf7180000396714:956857-957017 -		ACCAATGGACGAAGTCAGTCAACAGAGCACGCTTTCGAATGCATCAGCGGGTTAGTAAAAC--TG-TA--TAAAATAG----------TG----------AC----------AGTAGA--AACTAATA-GT-GTGTTC----TA---TTTTG-----TACAGCATCCGGCGAAGATCCTCAGTGCACCACACCAAAGTCGCGCAAAAACGAT
droKik1	scf7180000302247:509925-510084 +		GCCCATGGACGAAGTCAGTCAGCAGAGCACGCTATCGAATGCTTCAGCGGGTGAGTGCACC--AC----------GAC-------GC----T--T-CGA----ACC--GAATCACTTGATTAACG-TGT------TTG-CA---TCTCC-----CACAGCATCCGGCGAAGATCCACAATGCACCACACCAAAGTCGCGCAAAAATGAT
droFic1	scf7180000453912:1952661-1952829 +		GCCCATGGACGAAGTCAGTCAGCAGAGCAGTCTGTCAAATGCATCAGCGGGTGAGTAGAAGAGCGAAATATA-----T------AGCAT----------AAA----GA---AATTCCT--GACTTAAG-TTC------TT----T--TTTTGCGTAAACCAGCATCCGGCGAAGATCCACAGTGCACCACACCAAAGTCGCGCAAGAATGAT
droEle1	scf7180000491080:2754692-2754857 +		GCCCATGGACGACGTCAGTCAGCAGAGCACGCTCTCGAATGCATCAGCGGGTAAGTAGAAG--CCGGACTGC-----T------GGCCT----------TAA----GA---CATTTTC--GACTGACT-TAA------TTTATG-T--TTTTA-----CACAGCATCCGGCGAAGATCCACAATGCACCACACCAAAGTCGCGCAAGAATGAT
droRho1	scf7180000778039:38186-38353 +		CCCCATGGACGACGTCAGTCAGCAGAGCACGCTCTCGAATGCATCAGCGGGTAAGAAGAGC--CGGGATTTT-----A------GGCCT----------TTA----AA---GATTTTC--GACTAATTATTA------TTTATTTT--TAACT-----CACAGCATCCGGCGAAGATCCACAATGCACCACACCAAAGTCGCGCAAGAATGAT
droBia1	scf7180000302113:3895332-3895497 +		GCCCATGGACGAAGTCAGTCAGCAGAGCACGCTCTCGAATGCATCAGCGGGTGAGTACAGC--CGCAATGAA-----A------GGCTC----------GAA----GA---GATTGGC--AACTGATT-TTA------TTTCCC-A--TTTTA-----TGCAGCATCCGGCGAGGACCCACAATGCACCACACCAAAGTCGCGCAAGAATGAT
droTak1	scf7180000413103:19756-19829 +		----------GT-T----------T----------T----------

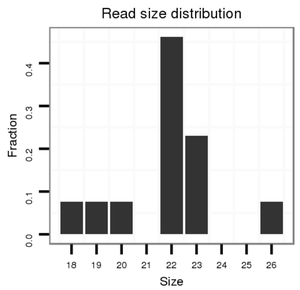
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_3826	**3:9802187-9802306 -**	**candidate-rescued**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

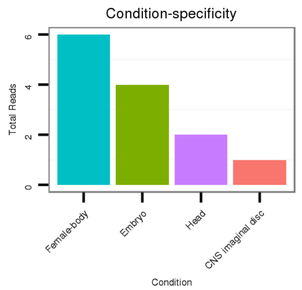
Legend: mature star mismatch in alignment mismatch in read

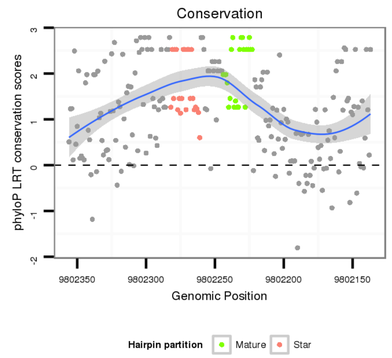
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dpse\GA24314-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
CGCTACTCAACACAACCGAAAGGAGTCCGCAGTATCAGTAGACAACACCAACAGCAGCAGCTGCCCAGTGCGCAGCTGCCGCTGTGCCGCTGTCGCCCTTGCCGCCACAACAGCAAACGACAGAGGCAACGGCAGCCACGCCAGTAGCAGCACCACCTACAACCACAACCACACTCGTCTCATCCGCCACCACGAGCATCATAGAAGCCTCCGCCTCGCCGC
*************************************************************(((((.....(((..(((((((..((((.(((((((...((((.........))))).))))))).))))..))))))..)))).....)))))*************************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	GSM343916 embryo	SRR902012 CNS imaginal disc	M062 head	SRR902010 ovaries	SRR902011 testis
22	0	1	3.00	3	1	0	2	0	0	0	0
28	0	1	2.00	2	0	0	0	2	0	0	0
27	0	1	2.00	2	0	0	0	0	0	2	0
23	0	1	1.00	1	1	0	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0	0
27	0	1	1.00	1	0	0	0	1	0	0	0
18	0	1	1.00	1	0	0	1	0	0	0	0
23	0	1	1.00	1	0	1	0	0	0	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0
29	0	1	1.00	1	0	0	0	0	0	0	1
20	0	1	1.00	1	0	0	0	1	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0	0
27	1	1	1.00	1	0	1	0	0	0	0	0
22	0	1	1.00	1	0	0	0	0	1	0	0
23	0	1	1.00	1	0	0	0	0	1	0	0
26	0	1	1.00	1	1	0	0	0	0	0	0
22	0	1	1.00	1	0	0	1	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0	0
21	0	1	1.00	1	0	1	0	0	0	0	0

Anti-sense strand reads

```
GCGATGAGTTGTGTTGGCTTTCCTCAGGCGTCATAGTCATCTGTTGTGGTTGTCGTCGTCGACGGGTCACGCGTCGACGGACACGGCGACACGCGGGAACGGCGGTGTTGTCGTTTGCTGTCTCCGTTGCCGTCGGTGCGGTCATCGTCGTGGTGGATGTTGGTGTTGGTGTGAGCAGAGTAGGCGGTGGTGCTCGTAGTATCTTCGGAGGCGGAGCGGCG
*************************************************************(((((.....(((..(((((((..((((.(((((((...((((.........))))).))))))).))))..))))))..)))).....)))))*************************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902011 testis	V112 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	3:9802137-9802356 -	dps_3826	CGCTAC-------T----------CAACACAACCGAAAGGAGTCCGCA-----GTATCAGTAG---------ACAAC----------ACCAA-----CAGCAG---CAGCTGCCCAGTGCGCAGCTGCCTGTG---CCGCTGTCGCCGTTGCCGCCACA---A---CAGCAAACGACAGAGGCAACGGCAGCC------ACGCCAGTAGCAG--------C---ACCA-CCTA----------CAAC----------CACA-ACCACACTCGTCTCAT--------CCGCCACCACGAGCATCATAGAAGCCTCCG-----CCT----------CGCCGC
droPer2	scaffold_4:5118111-5118339 -	dpe_2480	CGCTAC-------T----------CAGCACAACCGAAAGGAGTCCGGA-----GTATCAGTAG---------ACAAC----------ACCAA-----CAGCAG---CAGCTGCCCAGTGCGCAGCTGCCTGTG---CCGCTGTCGCCGTTGCCGCCACA---A---CAGCAAACGACAGAGGCAACGGCAGCC------ACGCCAGTAGCAG--------C---ACCA-CCTA----------CAAC----------CACA-ACACACTCGTCTCATCGCCCACTCGCCGCACCACGAGCATCATAGAAGCCTCCG-----CCT----------CGCCGC
droWil2	scf2_1100000005648:491-730 -		AGCAAGAATTGCAGCAACAACA---ACAAG-AGCA----------CAA-AACA--ACA-G-A-G---AGCA--------ACAAC---------AGCAGTGAGC---AACAGCAA---CAGCAGCAACGAATGCAGAGAAGACAAGAGCAAGATTGCAGCAACAACACAAGAGG----AAGACAACAAGAGCAGGAACA---ACAACAGCAGCAG--------C---AACAACAGCA--AG--------A---A----------CAA-AAC
droVir3	scaffold_12875:18068715-18068895 -	dvi_24649	AASA--------A----------A----------CAAAC-----------------CCAGCAAACAAGAAC---------CACAA-----CAGCAG---CAGCTGCTCAGTGCGCAGCTGCTGTG---CCGCTGTCGAATTGTG-------A---A--------GACAGAGGCAACGGCAGCAGCA---ACGCCAGCAGCAG--------C---TTCACATAG--TG--------CAATACA----------A----A----------A-------CAACAGCAGCAAGAACCTCCGCCTCCGGTGTCAGATTCCACAGCGCCAC
droMoj3	scaffold_6496:11689326-11689507 -	dmo_3164	AA----------A----------A----------A----------G-A-G---AGAAACCCAGCAACAACAAC---------A-CAA-----CAGCAG---CAGCTGCTCAGTGCGCAGCTGCTGTG---CCGCTGTCGAATTGTG-------A---A--------GACAGAGGCAACGGCAGCCGCA---ACGCCAGCAGCAG--------C---TTCACATAG--TG--------C----------A----A----------T----------CAATA-------T---A-CAAAAG-----AGAAACCTCCG-----TTTCAGAGTCAATAGGCCGC
droGri2	scaffold_15245:4197227-4197420 -	dgr_473	AAACAC--------A----------A----------A----------G-AA-A----G-A-G-AGAAAACCAACAA---C----------ACCAA-----CAGCAG---CAGCTGCCCAGTGCGCAGCTGCTGTG---CCGCTGTCGAATTGTG-------A---A--------GACAGAGGCAACGGCAGGGCAGCAAGCCAGCAGCG--------C---TTGCA----G----------CACATCATCA----------T-----CATCA----T----------CAATA-------CGAATCAATAAAG-----CAGAAG---TTG-----GGT-----CCACGAGGCCGC
droAna3	scaffold_13266:5014061-5014313 +	dan_91	CGCGAGCAGCAGATCACCACCACCAGCACCAGCGAGGAGGGAAAGGAATCGCGG-----GAA-----------ACAGAA---GGCCA---ACCAAGAGCAGCAGAAGCGCCCAGCTGCCCAGTGCGCAGCTGCTGTG---CCGCTGTCGCCGTTGCCGCAACA---A---CAGCAAACGACAGAGGCAACGGCAGCC------ACGCCAGCGCGCAG--------AGACACCGCCGAAGCATCAC--------A-----CCTCC----A----------C-----CGAGTAGCAGCAGCATCATAGAAGCCTCAG-----TTT----------CGCCGC
droBip1	scf7180000395751:823763-824000 +		CGCGAGCAGCAGATCACCACCACCAGCACCAGCGAGGAGGGAAAGGAATCGCGA-----GAA-----------ACAAGAGCAGGCCA---ACCAAGAGCAGCAGAAGCGCCCAGCTGCCCAGTGCGCAGCTGCTGTG---CCGCTGTCGCCGTTGCCGCCACA---T---CAGCAAACGACAGAGGCAACGGCAGCC------ACGCCAGCGCGCAG--------AGACTCCGCCGAAACAC--------C--G---ACC--------A-----CCTCC----T----------C-----CGAGTAGCACGAGCACATCATAGAAGCCTCCG-----TTT----------CGCCGC
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droSec2	scaffold_9:543236-543455	dse_1843	CGCGATCAGCAGATCACCACCACCAGCACATATAGCGAGCGAATGTGAAGGAATCGCCA-----GAGCAGTAGCAA----------A----------CAA------CAGAAG---CAACTCGCCAGTGCGCAGCTGCTGTG---CCGCTGTCGCCGTTGCCGCAACAACAA---CAGCAAACGCAGAAGGCAACGGCAGCAGCAGCA----------G--------C---ACCGCGCCGAGAGTCAGCCAAGGTATCC----------ACCTCCGTTT----T----------CGAGCACCACGAGCAGCATAGAAGCCTCGG-----TTT----------TGCCGC
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droEre2	scaffold_4845:11355664-11355880 +	der_1520	CGCGATCAGCAGATCACCACCACCAGCACATATAGCGAGCGTCAAAGGAATCGCCA-----GAGTGAGCA----------G----------CAA------CAGAAG---CAACTCGCCAGTGCGCAGCTGCTGTG---CCGCTGTCGCCGTTGCCGCAACAACA---CAGCAAACGCAGAAGGCAACGGCAGCAGCAGCA----------G--------C---ACCGCGCCGAGAGTCAGCCAAGGTATCC----------ACC----------T----------CCGGTTCCCTTAGCAGATAGAAGGCTCTGG-----CGT----------CGCCGC

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	PASS/FAIL
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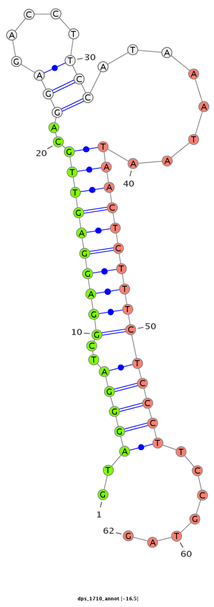
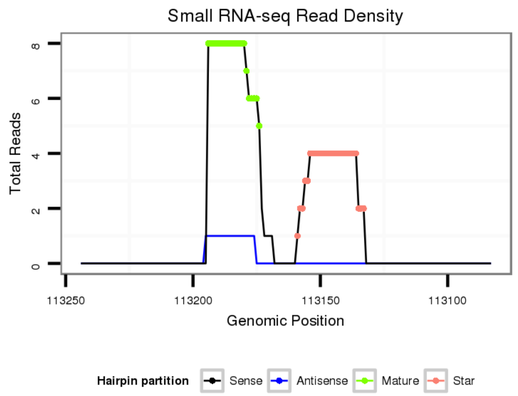
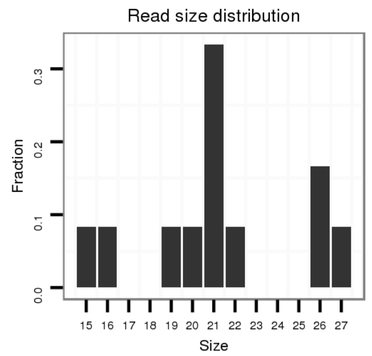
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_1710	**4_group5:113133-113194 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

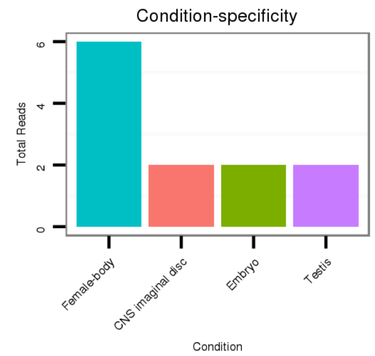
Legend: mature star mismatch in alignment mismatch in read

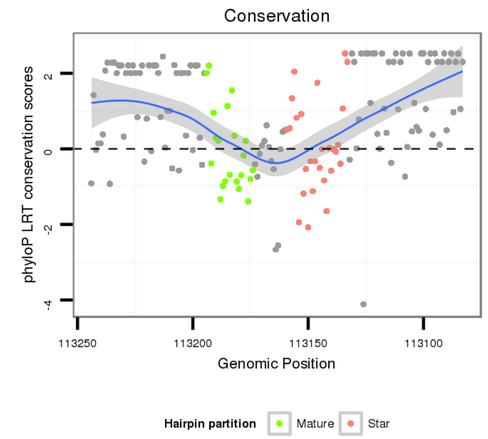
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dpse\GA10382-in]; CDS [Dpse\GA10382-cds]; CDS [Dpse\GA10382-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTGAGGCTGATGAAGGAGACGGTATTGAAGCTGCCGCCGCCACACTACAGGTAGGGATCGGAGGAGTTGCAGGAGACCTTCCATAAATAATAACTCTTTCTCCCTTCCGTAGAACCCTCAAATATCTGGCTGAGCATTTGTACAAGGTCTCGCAGCATCACG **********..(((((..(((((((((((..(((.....)))........)))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M059 embryo	SRR902011 testis	SRR902012 CNS imaginal disc	GSM343916 embryo	SRR902010 ovaries	V112 male body
.....GTAGGGATCGGAGGAGTTGCA.....	21	0	1	3.00	3	2	0	1	0	0	0	0
.....GTAGGGATCGGAGGAGTTGC.....	20	0	1	1.00	1	0	0	1	0	0	0	0
.....GTAGGGATCGGAGGAG.....	16	0	1	1.00	1	0	0	0	1	0	0	0
.....AATAATAACTCTTTCTCCCTTCCGTAG.....	27	0	1	1.00	1	0	0	0	0	1	0	0
.....TAACTCTTTCTCCCTTCCG.....	19	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAGGGATCGGAGGAGTTGCAG.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAGGGATCGGAGGA.....	15	0	1	1.00	1	0	0	0	1	0	0	0
.....AATAACTCTTTCTCCCTTCCG.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....ATAATAACTCTTTCTCCCTTCCGTAG.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....GTAGGGATCGGAGGAGTTGCAGGAGA.....	26	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

GACTCCGACTACTTCCTCTGCCATAACTTCGACGGCGGCGGTGTGATGTCCATCCCTAGCCTCCTCAACGTCCTCTGGAAGGTATTTATTATTGAGAAAGAGGGAAGGCATCTTGGGAGTTTATAGACCGACTCGTAAACATGTTCCAGAGCGTCGTAGTGC **********..(((((..(((((((((((..(((.....)))........)))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	M062 head	V112 male body	M059 embryo
.....CCATCCCTAGCCTCCTCAAC.....	20	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

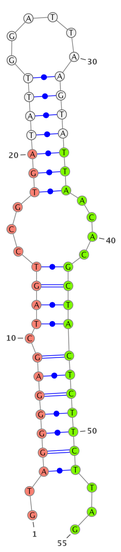
Re-alignment of all predicted orthologs

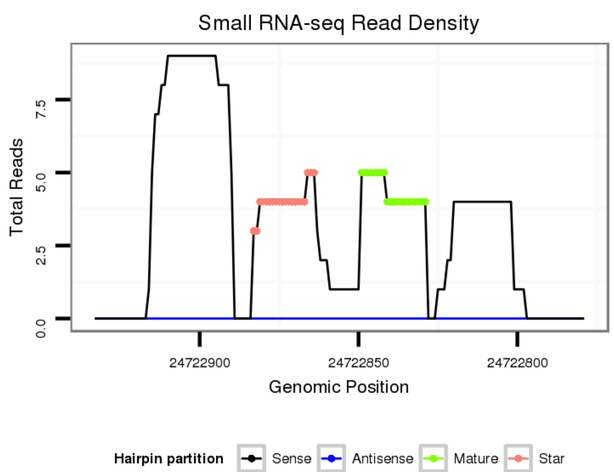
Species	Coordinate	ID	Alignment
dp5	4_group5:113083-113244 -	dps_1710	CTGAGGCTGATGAAGGAGACGGTATTGAAGCTGCCGCCGCCACACTACAGGTAGGGAT----------CGGAGGAGTTGCAGGAGACCTT-----CCATAAAT----------AATAACTCTTT----------CTCCCTTCCGTAGAACCCTCAAATATCTGGCTGAGCATTTGTACAAGGTCTCGCAGCATCACG
droPer2	scaffold_5:4613765-4613926 -	dpe_2492	CTGAGGCTGATGAAGGAGACGGTACTGAAGCTGCCGCCGCCACACTACAGGTAGGGAT----------CGGAGGAGTTGCAGGAGAACTT-----CCATAAAT----------AATAACTCTTT----------CTCCCTTCCGTAGAACCCTCAAATATCTGGCTGAGCATTTGTACAAGGTCTCGCAGCATCACG
droWil2	scf2_1100000004521:4000800-4000872 +		ATATT----------TGTTAC----------CTTT

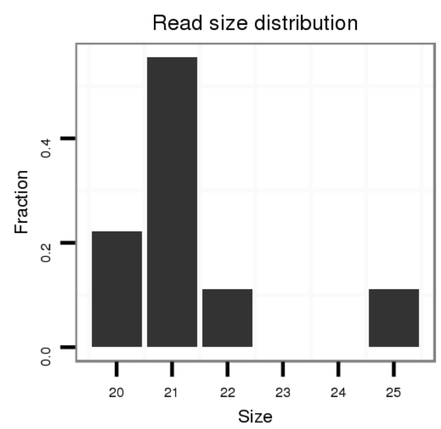
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dps_774	**2:24722829-24722883 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

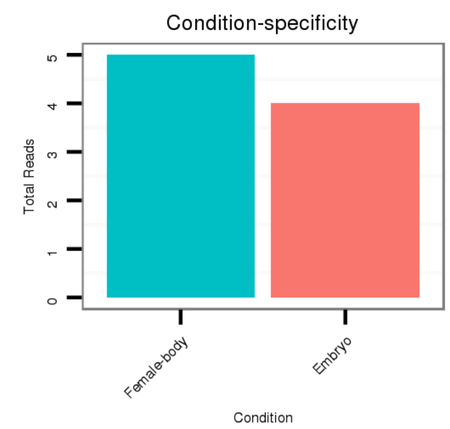
Legend: mature star mismatch in alignment mismatch in read

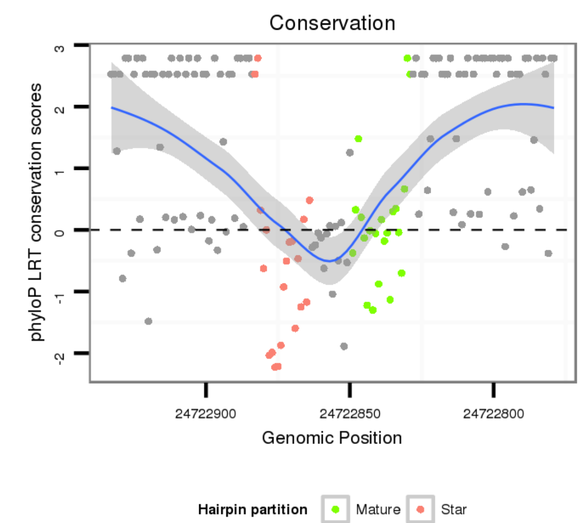
Predicted structure











dps_774.seed | 1.0.0.

Show Alternate Folds

Flybase annnotation

intron [Dpse\GA10588-in]; CDS [Dpse\GA10588-cds]; CDS [Dpse\GA10588-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGCGATACGTATCACCCTCGCAGGACGAAGAGCCGATTGAAGGCTACAAGGTAGGGGAGCTAGTCCGTGATATTGGATTAAGTATTAACACGCTACTCTTCTTAGGTTCGCATTTGGGAAACGGATCAGAACATGATTACTGCCAACAACACGAT **********..(((((((.((((...(((((((.....)))))))....)))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body	SRR902012 CNS imaginal disc	M059 embryo	GSM343916 embryo	SRR902011 testis	GSM444067 head
.....TTAACACGCTACTCTTCTTAGA.....	22	1	1	5.00	5	4	0	0	1	0	0
.....TTAACACGCTACTCTTCTTAG.....	21	0	1	4.00	4	3	0	1	0	0	0
.....CGCAGGACGAAGAGCCGATTGAAGGC.....	26	0	1	2.00	2	0	2	0	0	0	0
.....TTGGGAAACGGATCAGAAC.....	19	0	1	2.00	2	0	2	0	0	0	0
.....TTAACACGCTACTCTTCTTAGT.....	22	1	1	2.00	2	1	0	1	0	0	0
.....CGCAGGACGAAGAGCCGATTGAAGG.....	25	0	1	2.00	2	0	0	0	0	2	0
.....GTAGGGGAGCTAGTCCGTGA.....	20	0	1	2.00	2	0	0	0	2	0	0
.....ATTTGGGAAACGGATCAGAACATGA.....	25	0	1	1.00	1	0	1	0	0	0	0
.....TAACACGCTACTCTTCTTAGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTAGGGGAGCTAGTCCGTGAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGATATTGGATTAAGTATTAACACG.....	25	0	1	1.00	1	0	0	1	0	0	0
.....CGCATTTGGGAAACGGATCAGAAC.....	24	0	1	1.00	1	0	0	1	0	0	0
.....TTAACACGCTACTCTTCTTAGC.....	22	1	1	1.00	1	0	0	1	0	0	0
.....GCAGGACGAAGAGCCGATTGAAGGC.....	25	0	1	1.00	1	0	1	0	0	0	0
.....TCGCAGGACGAAGAGCCGATTGAAGGC.....	27	0	1	1.00	1	0	1	0	0	0	0
.....GACGAAGAGCCGATTGAAGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AGGGGAGCTAGTCCGTGATATT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGGACGAAGAGCCGATTGAAGGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GCAGGACGAAGAGCCGATTG.....	20	0	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

CCGCTATGCATAGTGGGAGCGTCCTGCTTCTCGGCTAACTTCCGATGTTCCATCCCCTCGATCAGGCACTATAACCTAATTCATAATTGTGCGATGAGAAGAATCCAAGCGTAAACCCTTTGCCTAGTCTTGTACTAATGACGGTTGTTGTGCTA **********..(((((((.((((...(((((((.....)))))))....)))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M040 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dp5	2:24722779-24722933 -	dps_774	GGCGATACGTATCACCCTCGCAGGACGAAGAGCCGATTGAAGGCTACAAGGTAGGGGAGC------TAGT----------CC------G----------TGATATTGGATTAAGTATTAACACGCT-------ACTC-TTCTTAGGTTCGCATTTGGGAAACGGATCAGAACATGATTACTGCCAACAACACGAT
droPer2	scaffold_3:7365150-7365304 -	dpe_2491	GGCGATACGTATCACCCTCGCAGGACGAAGAGCCGATTGAAGGCTACAAGGTAGGGGAGC------TAGT----------CC------G----------TGATATTGGATTAAGTATTAACACGCT-------ACTC-TTCTTAGGTTCGCATTTGGGAAACGGATCAGAACATGATTACTGCCAACAACACGAT
droWil2	scf2_1100000004943:3056454-3056620 -		GGCGATATGTATCTCCCTCGCAGGACGAGGAGCCCATTGAAGGCTATAAGGTAAGCATAT------G---------AAATATATCAATGTTGATCTAATCTAAAGTAAAACTCTG----------CAATGTT--------CTT-ATTTTAGGTACGCATTTGGGAAACGGATCAGAACATGATCACTGCCAATAACACAAT
droVir3	scaffold_13047:11826677-11826839 -		GGCGTTACGTATCACCAGCTCAAGATGAGGAACCCATTGAGGGCTATAAGGTATAAAAGC------CTGT----------GAA-----T-A------TGCTTTAGG-----CAAC--CATATATAAAATGTAATTCCCTTT-TTGGCAGGTACGCATTTGGGAGACAGATCAAAATATGATCACTGCCAACAATAGAAT
droMoj3	scaffold_6540:29947812-29947975 +		GGCGTTATGTATCGCCGGCGCAAGATGAAGAGCCACTGCCTGGCTATAAGGTATGGATTA------TGCT---T----------TTA-----ATGTGTCAACGGCAGGCA-----ATGT--TAAATATTATTTC-------AATT-TTCACAGGTTCGCATTTGGGACACGATCAGAATATGATCACTGCCAAGCATAGTAT
droGri2	scaffold_14624:1933647-1933815 -		GGCGATATGTTTGCCAGCGGCAGGATGAGGAGCCCATTGAAGGCTATAAGGTTGGCTTCAACAAAATGATGCCTTAAC----------AAA-----A-------ATATCAAAA----------ACTAATG-TAT-CGATTTATA-TTCACAGGTGCGCATTTGGGAGACCGATCAGAATATGATAACAGCCAACAATTACGAT
droAna3	scaffold_13340:11205415-11205571 +		GGCGCTACGTATCGCCCTCGCAGGATGAGGAGCCGATCGAAGGCTATAAGGTGAGTGTCC------TTGA----------TCC-----T-------TGAAAAAAT-----CATAAATCATAAACACTTT-------TTAT-ATGATAGGTTCGTATTTGGGAGACGGACCAAAACATGATAACAGCCAACAATTACCAT
droBip1	scf7180000396691:116173-116329 +		GGCGCTACGTATCGCCCTCGCAGGATGAGGAACCGGTCGAAGGCTATAAGGTAAGCAGAA------A---------AAATATC----------TC------T----------TAAAGCAACTTTAACTAATAATGCCTT--------CA-TTGTTAGGTTCGTATTTGGGAGACGGACCAAAACATGATCACAGCCAACAATAGCAT
droKik1	scf7180000302475:485175-485331 -		GGCGATATGTTTGCCCCTCGCAGGACGAGGAACCCATCGAAGGTTACAAGGTAAGCTTGG------TAGC----------AAAGCACCG----------CGAAA-------ATAAGGCAATAACATCTC-------AGCC-TGTTTAGGTTCGCATTTGGGAGACGGATCAGAACATGATCACAGCCAACAATTACCAT
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droEre2	scaffold_4770:556223-556377 +		GGCGATATGTTTGCCCCTCGCAGGACGAGGAACCAGTCGAGGGTTATAAGGTACGCCGGC------CGGC----------TCA-----G-------TGACAAAGA-----ATAT--CTATTACAATTTA-------AAAC-TTTTTAGGTTCGCATTTGGGAAACGGACCAGAACATGATCACGGCAAACAATAGCAT

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crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2